

# SEQUENCE LISTING

<110> Gilbert, Michel  
Wakarchuk, Warren W.  
National Research Council of Canada

<120> Campylobacter Glycosyltransferases for Biosynthesis of  
Gangliosides and Ganglioside Mimics

<130> 019633-000111US

<140> US 09/816,028

<141> 2001-03-21

<150> US 60/118,213

<151> 1999-02-01

<150> US 09/495,406

<151> 2000-01-31

<160> 49

<170> PatentIn Ver. 2.1

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<223> 11.5 kb PCR product from C. jejuni OH4384  
including LOS biosynthesis locus

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strain OH4384 (ORF 7a of lipooligosaccharide (LOS)  
biosynthesis locus)

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Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala	
210 215 220	
cca aat tta aat tca aat ttt atc ata caa gaa aaa aat aac tac act	720
Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr	
225 230 235 240	

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aaa gat ata ctc ata cct tct agt gag gct tat gga aaa ttt tca aaa 768
Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys
                245                250                255

aat att aat ttt aaa aaa ata aaa att aaa gaa aat att tat tac aag 816
Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Ile Tyr Tyr Lys
                260                265                270

ttg ata aaa gat cta tta aga tta cct agt gat ata aag cat tat ttc 864
Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe
                275                280                285

aaa gga aaa taa 876
Lys Gly Lys
                290

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<210> 3
<211> 291
<212> PRT
<213> Campylobacter jejuni

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<220>
<223> bifunctional alpha-2,3/alpha 2,8-sialyltransferase
      Campylobacter sialyltransferase II (cstII) from C. jejuni
      strain OH4384 (ORF 7a of lipooligosaccharide (LOS)
      biosynthesis locus)

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<400> 3
Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile
 1          5          10          15
Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln
          20          25          30
Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Ala Val
          35          40          45
Phe Tyr Asn Pro Ile Leu Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His
          50          55          60
Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn
          65          70          75          80
Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr
          85          90          95
Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu
          100          105          110
Lys Asp Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln
          115          120          125
Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly
          130          135          140
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser
          145          150          155          160
Ser Tyr Ala Phe Asp Thr Lys Gln Lys Asn Leu Leu Lys Leu Ala Pro
          165          170          175
Asn Phe Lys Asn Asp Asn Ser His Tyr Ile Gly His Ser Lys Asn Thr
          180          185          190
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu
          195          200          205
Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala
          210          215          220
Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr
          225          230          235          240
Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys
          245          250          255

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Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Ile Tyr Tyr Lys  
260 265 270  
Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe  
275 280 285  
Lys Gly Lys  
290

<210> 4  
<211> 876  
<212> DNA  
<213> Campylobacter jejuni

<220>  
<221> CDS  
<222> (1)..(876)  
<223> bifunctional alpha-2,3/alpha 2,8-sialyltransferase  
Campylobacter sialyltransferase II (cstII) from C. jejuni  
serotype O:10 (ORF 7a of lipooligosaccharide (LOS)  
biosynthesis locus)

<400> 4  
atg aaa aaa gtt att att gct gga aat gga cca agt tta aaa gaa att 48  
Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile  
1 5 10 15  
gat tat tca agg cta cca aat gat ttt gat gta ttt aga tgc aat caa 96  
Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln  
20 25 30  
ttt tat ttt gaa gat aaa tac tat ctt ggt aaa aaa ttc aaa gca gta 144  
Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Phe Lys Ala Val  
35 40 45  
ttt tac aat cct ggt ctt ttt ttt gaa caa tac tac act tta aaa cat 192  
Phe Tyr Asn Pro Gly Leu Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His  
50 55 60  
tta atc caa aat caa gaa tat gag acc gaa cta att atg tgt tct aat 240  
Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn  
65 70 75 80  
tac aac caa gct cat cta gaa aat gaa aat ttt gta aaa act ttt tac 288  
Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr  
85 90 95  
gat tat ttt cct gat gct cat ttg gga tat gat ttt ttt aaa caa ctt 336  
Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu  
100 105 110  
aaa gaa ttt aat gct tat ttt aaa ttt cac gaa att tat ctc aat caa 384  
Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Leu Asn Gln  
115 120 125  
aga att acc tca gga gtc tat atg tgt gca gta gct ata gcc cta gga 432  
Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly  
130 135 140

tac aaa gaa att tat ctt tct gga att gat ttt tat caa aat ggg tca	480
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser	
145 150 155 160	
tct tat gct ttt gat acc aaa caa gaa aat ctt tta aaa ctg gct cct	528
Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro	
165 170 175	
gat ttt aaa aat gat cgc tca cac tat atc gga cat agt aaa aat aca	576
Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr	
180 185 190	
gat ata aaa gct tta gaa ttt cta gaa aaa act tac aaa ata aaa cta	624
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu	
195 200 205	
tat tgc tta tgt cct aac agt ctt tta gca aat ttt ata gaa cta gcg	672
Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala	
210 215 220	
cca aat tta aat tca aat ttt atc ata caa gaa aaa aat aac tac act	720
Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr	
225 230 235 240	
aaa gat ata ctc ata cct tct agt gag gct tat gga aaa ttt tca aaa	768
Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys	
245 250 255	
aat att aat ttt aaa aaa ata aaa att aaa gaa aat att tat tac aag	816
Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Ile Tyr Tyr Lys	
260 265 270	
ttg ata aaa gat cta tta aga tta cct agt gat ata aag cat tat ttc	864
Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe	
275 280 285	
aaa gga aaa taa	876
Lys Gly Lys	
290	

<210> 5

<211> 291

<212> PRT

<213> Campylobacter jejuni

<220>

<223> bifunctional alpha-2,3/alpha 2,8-sialyltransferase  
Campylobacter sialyltransferase II (cstII) from C. jejuni  
serotype O:10 (ORF 7a of lipooligosaccharide (LOS)  
biosynthesis locus)

<400> 5

Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile	
1 5 10 15	
Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln	
20 25 30	
Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Phe Lys Ala Val	
35 40 45	
Phe Tyr Asn Pro Gly Leu Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His	
50 55 60	



Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn  
 65 70 75 80  
 Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr  
 85 90 95  
 Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu  
 100 105 110  
 Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Leu Asn Gln  
 115 120 125  
 Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly  
 130 135 140  
 Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser  
 145 150 155 160  
 Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro  
 165 170 175  
 Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr  
 180 185 190  
 Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu  
 195 200 205  
 Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala  
 210 215 220  
 Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr  
 225 230 235 240  
 Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys  
 245 250 255  
 Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Ile Tyr Tyr Lys  
 260 265 270  
 Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe  
 275 280 285  
 Lys Gly Lys  
 290

<210> 6

<211> 876

<212> DNA

<213> Campylobacter jejuni

<220>

<221> CDS

<222> (1)..(876)

<223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II  
(cstII) from C. jejuni serotype O:41

<400> 6

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 Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile  
 1 5 10 15

gat tat tca aga cta cca aat gat ttt gat gta ttt aga tgc aat caa 96  
 Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln  
 20 25 30

ttt tat ttt gaa gat aaa tac tat ctt ggt aaa aaa tgc aaa gca gta 144  
 Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Ala Val  
 35 40 45

ttt tac aat cct agt ctt ttt ttt gaa caa tac tac act tta aaa cat 192  
 Phe Tyr Asn Pro Ser Leu Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His  
 50 55 60

tta atc caa aat caa gaa tat gag acc gaa cta atc atg tgt tct aat	240
Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn	
65 70 75 80	
ttt aac caa gct cat cta gaa aat caa aat ttt gta aaa act ttt tac	288
Phe Asn Gln Ala His Leu Glu Asn Gln Asn Phe Val Lys Thr Phe Tyr	
85 90 95	
gat tat ttt cct gat gct cat ttg gga tat gat ttt ttc aaa caa ctt	336
Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu	
100 105 110	
aaa gaa ttc aat gct tat ttt aaa ttt cac gaa att tat ttc aat caa	384
Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln	
115 120 125	
aga att acc tca ggg gtc tat atg tgc aca gta gcc ata gcc cta gga	432
Arg Ile Thr Ser Gly Val Tyr Met Cys Thr Val Ala Ile Ala Leu Gly	
130 135 140	
tac aaa gaa att tat ctt tcg gga att gat ttt tat caa aat gga tca	480
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser	
145 150 155 160	
tct tat gct ttt gat acc aaa caa aaa aat ctt tta aaa ttg gct cct	528
Ser Tyr Ala Phe Asp Thr Lys Gln Lys Asn Leu Leu Lys Leu Ala Pro	
165 170 175	
aat ttt aaa aat gat aat tca cac tat atc gga cat agt aaa aat aca	576
Asn Phe Lys Asn Asp Asn Ser His Tyr Ile Gly His Ser Lys Asn Thr	
180 185 190	
gat ata aaa gct tta gaa ttt cta gaa aaa act tac gaa ata aag cta	624
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Glu Ile Lys Leu	
195 200 205	
tat tgt tta tgt cct aac agt ctt tta gca aat ttt ata gaa cta gcg	672
Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala	
210 215 220	
cca aat tta aat tca aat ttt atc ata caa gaa aaa aat aac tat act	720
Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr	
225 230 235 240	
aaa gat ata ctc ata cct tct agt gag gct tat gga aaa ttt aca aaa	768
Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Thr Lys	
245 250 255	
aat att aat ttt aaa aaa ata aaa att aaa gaa aat att tat tac aag	816
Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Ile Tyr Tyr Lys	
260 265 270	
ttg ata aaa gat cta tta aga tta cct agt gat ata aag cat tat ttc	864
Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe	
275 280 285	
aaa gga aaa taa	876
Lys Gly Lys	
290	

<210> 7  
 <211> 291  
 <212> PRT  
 <213> Campylobacter jejuni

<220>  
 <223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II  
 (cstII) from C. jejuni serotype O:41

<400> 7  
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 1 5 10 15  
 Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln  
 20 25 30  
 Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Ala Val  
 35 40 45  
 Phe Tyr Asn Pro Ser Leu Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His  
 50 55 60  
 Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn  
 65 70 75 80  
 Phe Asn Gln Ala His Leu Glu Asn Gln Asn Phe Val Lys Thr Phe Tyr  
 85 90 95  
 Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu  
 100 105 110  
 Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln  
 115 120 125  
 Arg Ile Thr Ser Gly Val Tyr Met Cys Thr Val Ala Ile Ala Leu Gly  
 130 135 140  
 Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser  
 145 150 155 160  
 Ser Tyr Ala Phe Asp Thr Lys Gln Lys Asn Leu Leu Lys Leu Ala Pro  
 165 170 175  
 Asn Phe Lys Asn Asp Asn Ser His Tyr Ile Gly His Ser Lys Asn Thr  
 180 185 190  
 Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Glu Ile Lys Leu  
 195 200 205  
 Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala  
 210 215 220  
 Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr  
 225 230 235 240  
 Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Thr Lys  
 245 250 255  
 Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Ile Tyr Tyr Lys  
 260 265 270  
 Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe  
 275 280 285  
 Lys Gly Lys  
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<210> 8  
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 <212> DNA  
 <213> Campylobacter jejuni

<220>  
 <221> CDS  
 <222> (1)..(876)  
 <223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II  
 (CstII) from C. jejuni O:19

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gat tat tca agg cta cca aat gat ttt gat gta ttt aga tgt aat caa	96
Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln	
20 25 30	
ttt tat ttt gaa gat aaa tac tat ctt ggt aaa aaa tgc aaa gca gtg	144
Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Ala Val	
35 40 45	
ttt tac acc cct aat ttc ttc ttt gag caa tac tac act tta aaa cat	192
Phe Tyr Thr Pro Asn Phe Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His	
50 55 60	
tta atc caa aat caa gaa tat gag acc gaa cta att atg tgt tct aat	240
Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn	
65 70 75 80	
tac aac caa gct cat cta gaa aat gaa aat ttt gta aaa act ttt tac	288
Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr	
85 90 95	
gat tat ttt cct gat gct cat ttg gga tat gat ttt ttt aaa caa ctt	336
Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu	
100 105 110	
aaa gaa ttt aat gct tat ttt aaa ttt cac gaa att tat ttc aat caa	384
Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln	
115 120 125	
aga att acc tca ggg gtc tat atg tgt gca gta gcc ata gcc cta gga	432
Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly	
130 135 140	
tac aaa gaa att tat ctt tcg gga att gat ttt tat caa aat ggg tca	480
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser	
145 150 155 160	
tct tat gct ttt gat acc aaa caa gaa aat ctt tta aaa cta gcc cct	528
Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro	
165 170 175	
gat ttt aaa aat gat cgc tcg cac tat atc gga cat agt aaa aat aca	576
Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr	
180 185 190	
gat ata aaa gct tta gaa ttt cta gaa aaa act tac aaa ata aaa cta	624
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu	
195 200 205	
tat tgc tta tgt cct aat agt ctt tta gca aat ttt ata gaa cta gcg	672
Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala	
210 215 220	
cca aat tta aat tca aat ttt atc ata caa gaa aaa aat aac tac act	720
Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr	
225 230 235 240	

aaa gat ata ctc ata cct tct agt gag gct tat gga aaa ttt tca aaa 768  
 Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys  
                   245                                  250                                  255

aat att aat ttt aaa aaa ata aaa att aaa gaa aat gtt tat tac aag 816  
 Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Val Tyr Tyr Lys  
                   260                                  265                                  270

ttg ata aaa gat cta tta aga tta cct agt gat ata aag cat tat ttc 864  
 Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe  
                   275                                  280                                  285

aaa gga aaa taa 876  
 Lys Gly Lys  
           290

<210> 9

<211> 291

<212> PRT

<213> Campylobacter jejuni

<220>

<223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II  
 (CstII) from C. jejuni O:19

<400> 9

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   1                                  5                                  10                                  15  
 Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln  
                   20                                  25                                  30  
 Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Ala Val  
                   35                                  40                                  45  
 Phe Tyr Thr Pro Asn Phe Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His  
                   50                                  55                                  60  
 Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn  
                   65                                  70                                  75                                  80  
 Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr  
                   85                                  90                                  95  
 Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu  
                   100                                  105                                  110  
 Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln  
                   115                                  120                                  125  
 Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly  
                   130                                  135                                  140  
 Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser  
                   145                                  150                                  155                                  160  
 Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro  
                   165                                  170                                  175  
 Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr  
                   180                                  185                                  190  
 Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu  
                   195                                  200                                  205  
 Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala  
                   210                                  215                                  220  
 Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr  
                   225                                  230                                  235                                  240  
 Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys  
                   245                                  250                                  255  
 Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Val Tyr Tyr Lys  
                   260                                  265                                  270

Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe  
           275                                  280                                  285  
 Lys Gly Lys  
       290

<210> 10  
 <211> 294  
 <212> PRT  
 <213> Campylobacter jejuni

<220>  
 <223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II  
       (CstII) from C. jejuni strain NCTC 11168

<400> 10  
 Met Ser Met Asn Ile Asn Ala Leu Val Cys Gly Asn Gly Pro Ser Leu  
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 Lys Asn Ile Asp Tyr Lys Arg Leu Pro Lys Gln Phe Asp Val Phe Arg  
                                   20                                  25                                  30  
 Cys Asn Gln Phe Tyr Phe Glu Asp Arg Tyr Phe Val Gly Lys Asp Val  
                                   35                                  40                                  45  
 Lys Tyr Val Phe Phe Asn Pro Phe Val Phe Phe Glu Gln Tyr Tyr Thr  
                                   50                                  55                                  60  
 Ser Lys Lys Leu Ile Gln Asn Glu Glu Tyr Asn Ile Glu Asn Ile Val  
   65                                  70                                  75                                  80  
 Cys Ser Thr Ile Asn Leu Glu Tyr Ile Asp Gly Phe Gln Phe Val Asp  
                                   85                                  90                                  95  
 Asn Phe Glu Leu Tyr Phe Ser Asp Ala Phe Leu Gly His Glu Ile Ile  
                                   100                                  105                                  110  
 Lys Lys Leu Lys Asp Phe Phe Ala Tyr Ile Lys Tyr Asn Glu Ile Tyr  
                                   115                                  120                                  125  
 Asn Arg Gln Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Thr Ala Val  
   130                                  135                                  140  
 Ala Leu Gly Tyr Lys Ser Ile Tyr Ile Ser Gly Ile Asp Phe Tyr Gln  
   145                                  150                                  155                                  160  
 Asp Thr Asn Asn Leu Tyr Ala Phe Asp Asn Asn Lys Lys Asn Leu Leu  
                                   165                                  170                                  175  
 Asn Lys Cys Thr Gly Phe Lys Asn Gln Lys Phe Lys Phe Ile Asn His  
                                   180                                  185                                  190  
 Ser Met Ala Cys Asp Leu Gln Ala Leu Asp Tyr Leu Met Lys Arg Tyr  
                                   195                                  200                                  205  
 Asp Val Asn Ile Tyr Ser Leu Asn Ser Asp Glu Tyr Phe Lys Leu Ala  
   210                                  215                                  220  
 Pro Asp Ile Gly Ser Asp Phe Val Leu Ser Lys Lys Pro Lys Lys Tyr  
   225                                  230                                  235                                  240  
 Ile Asn Asp Ile Leu Ile Pro Asp Lys Tyr Ala Gln Glu Arg Tyr Tyr  
                                   245                                  250                                  255  
 Gly Lys Lys Ser Arg Leu Lys Glu Asn Leu His Tyr Lys Leu Ile Lys  
                                   260                                  265                                  270  
 Asp Leu Ile Arg Leu Pro Ser Asp Ile Lys His Tyr Leu Lys Glu Lys  
                                   275                                  280                                  285  
 Tyr Ala Asn Lys Asn Arg  
       290

<210> 11  
 <211> 873  
 <212> DNA  
 <213> Campylobacter jejuni

<220>

<221> CDS

<222> (1)..(873)

<223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II  
(CstII) from C. jejuni O:4

<400> 11

atg aaa aaa gtt att att gct gga aat gga cca agt tta aaa gaa att	48
Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile	
1 5 10 15	
gat tat tca agg cta cca aat gat ttt gat gta ttt aga tgt aat caa	96
Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln	
20 25 30	
ttt tat ttt gaa gat aaa tac tat ctt ggt aaa aaa tgc aaa gca gtg	144
Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Ala Val	
35 40 45	
ttt tac acc cct ggt ttc ttc ttt gag caa tac tac act tta aaa cat	192
Phe Tyr Thr Pro Gly Phe Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His	
50 55 60	
tta atc caa aat caa gaa tat gag acc gaa cta att atg tgt tct aat	240
Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn	
65 70 75 80	
tac aac caa gct cat cta gaa aat gaa aat ttt gta aaa act ttt tac	288
Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr	
85 90 95	
gat tat ttt cct gat gct cat ttg gga tat gat ttt ttt aaa caa ctt	336
Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu	
100 105 110	
aaa gaa ttt aat gct tat ttt aaa ttt cac gaa att tat ttc aat caa	384
Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln	
115 120 125	
aga att acc tca ggg gtc tat atg tgt gca gta gcc ata gcc cta gga	432
Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly	
130 135 140	
tac aaa gaa att tat ctt tcg gga att gat ttt tat caa aat ggg tca	480
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser	
145 150 155 160	
tct tat gct ttt gat acc aaa caa gaa aat ctt tta aaa cta gcc cct	528
Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro	
165 170 175	
gat ttt aaa aat gat cgc tca cac tat atc gga cat agt aaa aat aca	576
Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr	
180 185 190	
gat ata aaa gct tta gaa ttt cta gaa aaa act tac aaa ata aaa cta	624
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu	
195 200 205	

tat tgc tta tgt cct aac agt ctt tta gca aat ttt ata gaa cta gcg	672
Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala	
210 215 220	
cca aat tta aat tca aat ttt atc ata caa gaa aaa aat aac tac act	720
Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr	
225 230 235 240	
aaa gat ata ctc ata cct tct agt gag gct tat gga aaa ttt tca aaa	768
Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys	
245 250 255	
aat att aat ttt aaa aaa ata aaa att aaa gaa aat gtt tat tac aag	816
Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Val Tyr Tyr Lys	
260 265 270	
ttg ata aaa gat cta tta aga tta cct agt gat ata aag cat tat ttc	864
Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe	
275 280 285	
aaa gga aaa	873
Lys Gly Lys	
290	

<210> 12

<211> 291

<212> PRT

<213> Campylobacter jejuni

<220>

<223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II  
(CstII) from C. jejuni O:4

<400> 12

Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile	
1 5 10 15	
Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln	
20 25 30	
Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Ala Val	
35 40 45	
Phe Tyr Thr Pro Gly Phe Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His	
50 55 60	
Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn	
65 70 75 80	
Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr	
85 90 95	
Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu	
100 105 110	
Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln	
115 120 125	
Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly	
130 135 140	
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser	
145 150 155 160	
Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro	
165 170 175	
Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr	
180 185 190	
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu	
195 200 205	



Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala  
 210 215 220  
 Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr  
 225 230 235 240  
 Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys  
 245 250 255  
 Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Val Tyr Tyr Lys  
 260 265 270  
 Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe  
 275 280 285  
 Lys Gly Lys  
 290

<210> 13  
 <211> 873  
 <212> DNA  
 <213> *Campylobacter jejuni*

<220>  
 <221> CDS  
 <222> (1)..(873)  
 <223> *Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II*  
 (CstII) from *C. jejuni* O:36

<400> 13  
 atg aaa aaa gtt att att gct gga aat gga cca agt tta aaa gaa att 48  
 Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile  
 1 5 10 15  
 gat tat tca agg cta cca aat gat ttt gat gta ttt aga tgt aat caa 96  
 Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln  
 20 25 30  
 ttt tat ttt gaa gat aaa tac tat ctt ggt aaa aaa tgc aaa aca gtg 144  
 Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Thr Val  
 35 40 45  
 ttt tac acc cct aat ttc ttc ttt gag caa tac tac act tta aaa cat 192  
 Phe Tyr Thr Pro Asn Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His  
 50 55 60  
 tta atc caa aat caa gaa tat gag acc gaa cta att atg tgt tct aat 240  
 Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn  
 65 70 75 80  
 tac aac caa gct cat cta gaa aat gaa aat ttt gta aaa act ttt tac 288  
 Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr  
 85 90 95  
 gat tat ttt cct gat gct cat ttg gga tat gat ttt ttt aaa caa ctt 336  
 Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu  
 100 105 110  
 aaa gaa ttt aat gct tat ttt aaa ttt cac gaa att tat ttc aat caa 384  
 Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln  
 115 120 125

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aga att acc tca ggg gtc tat atg tgt gca gta gcc ata gcc cta gga 432
Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly
130 135 140

tac aaa gaa att tat ctt tgc gga att gat ttt tat caa aat ggg tca 480
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser
145 150 155 160

tct tat gct ttt gat acc aaa caa gaa aat ctt tta aaa cta gcc cct 528
Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro
165 170 175

gat ttt aaa aat gat cgc tca cac tat atc gga cat agt aaa aat aca 576
Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr
180 185 190

gat ata aaa gct tta gaa ttt cta gaa aaa act tac aaa ata aaa cta 624
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu
195 200 205

tat tgc tta tgt cct aat agt ctt tta gca aat ttt ata gaa cta gcg 672
Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala
210 215 220

cca aat tta aat tca aat ttt atc ata caa gaa aaa aat aac tac act 720
Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr
225 230 235 240

aaa gat ata ctc ata cct tct agt gag gct tat gga aaa ttt tca aaa 768
Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys
245 250 255

aat att aat ttt aaa aaa ata aaa att aaa gaa aat gtt tat tac aag 816
Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Val Tyr Tyr Lys
260 265 270

ttg ata aaa gat cta tta aga tta cct agt gat ata aag cat tat ttc 864
Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe
275 280 285

aaa gga aaa 873
Lys Gly Lys
290

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<210> 14
<211> 291
<212> PRT
<213> Campylobacter jejuni

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<220>
<223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II
(CstII) from C. jejuni O:36

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<400> 14
Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile
1 5 10 15
Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln
20 25 30

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Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Thr Val  
           35                          40                          45  
 Phe Tyr Thr Pro Asn Phe Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His  
           50                          55                          60  
 Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn  
           65                          70                          75                          80  
 Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr  
                           85                          90                          95  
 Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu  
                          100                         105                         110  
 Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln  
                          115                         120                         125  
 Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly  
           130                         135                         140  
 Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser  
           145                         150                         155                         160  
 Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro  
                          165                         170                         175  
 Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr  
                          180                         185                         190  
 Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu  
                          195                         200                         205  
 Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala  
           210                         215                         220  
 Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr  
           225                         230                         235                         240  
 Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys  
                          245                         250                         255  
 Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Val Tyr Tyr Lys  
                          260                         265                         270  
 Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe  
           275                         280                         285  
 Lys Gly Lys  
           290

<210> 15  
 <211> 1170  
 <212> DNA  
 <213> *Campylobacter jejuni*

<220>  
 <223> glycosyltransferase from *C. jejuni* strain OH4384  
 (ORF 4a of lipooligosaccharide (LOS) biosynthesis  
 locus)

<400> 15  
 atgaagaaaa taggtgtagt tataccaatc tataatgtag aaaaatattt aagagaatgt 60  
 ttagatagcg ttatcaatca aacttatact aacttagaaa tcatacttgt caatgatggg 120  
 agcacagatg aacactcact caatattgca aaagaatata ccttaaaaga taaaagaata 180  
 actctttttg ataagaaaaa tgggggttta agttcagcta gaaatatagg tatagaatac 240  
 tttagcgggg aatataaatt aaaaaacaaa actcaacata taaaagaaaa ttctttaata 300  
 gaatttcaat tggatggtaa taatccttat aatatatata aagcatataa aagctctcaa 360  
 gcttttaata atgaaaaaga tttaaccaat ttactttacc ctagtataga ttatattata 420  
 ttcttagata gtgataatta ttggaaacta aactgcatag aagaatgcgt tataagaatg 480  
 aaaaatgtgg atgtattgtg gtttgaccat gattgcacct atgaagacaa tataaaaaat 540  
 aagcacaaaa aaacaaggat ggaaattttt gattttaaaa aagaatgtat aatcactcca 600  
 aaagaatatg caaatcgagc attaatgtga ggatctagag atatttcttt tggatggaat 660  
 ggaatgattg attttaattt tttaaagcaa attaaactta aattttataaa tttttatttc 720  
 aatgaagata tacacttttg gataattttg tttgctagtg ctaataaaat ttatgtttta 780  
 tcacaaaagt tgtattttgtg tcgtttaaga gcaaacagta tatcaaatca tgataagaag 840

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attacaaaag caaatgtgtc agagtatttt aaagatatat atgaaacttt cggggaaaaac 900
gctaaggaag caaaaaatta tttaaaagca gcaagcaggg ttataactgc tttaaaattg 960
atagaatttt tttaaagatca aaaaaacgaa aatgcacttg ctataaaaga aacattttta 1020
ccttgctatg ccaaaaaagc tttaatgatt aaaaaattta aaaaagatcc tttaaattta 1080
aaggaacaat tagttttaat taaacctttt attcaaaca aacttcctta tgatatttgg 1140
aaattttggc aaaaaataaa aaatatatta 1170

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<210> 16

<211> 1044

<212> DNA

<213> Campylobacter jejuni

<220>

<221> CDS

<222> (1)..(1044)

<223> beta-1,4 N-acetylgalactosaminyl (GalNAc)  
transferase from C. jejuni strain OH4384 (ORF 5a  
of lipooligosaccharide (LOS) biosynthesis locus)

<400> 16

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atg cta ttt caa tca tac ttt gtg aaa ata att tgc tta ttc atc cct 48
Met Leu Phe Gln Ser Tyr Phe Val Lys Ile Ile Cys Leu Phe Ile Pro
  1             5             10             15

ttt aga aaa att aga cat aaa ata aaa aaa aca ttt tta cta aaa aac 96
Phe Arg Lys Ile Arg His Lys Ile Lys Lys Thr Phe Leu Leu Lys Asn
      20             25             30

ata caa cga gat aaa atc gat tct tat tta cca aaa aaa act ctt gtg 144
Ile Gln Arg Asp Lys Ile Asp Ser Tyr Leu Pro Lys Lys Thr Leu Val
      35             40             45

caa att aat aaa tac aac aat gaa gat tta att aaa ctt aat aaa gct 192
Gln Ile Asn Lys Tyr Asn Asn Glu Asp Leu Ile Lys Leu Asn Lys Ala
      50             55             60

att ata ggg gag ggg cat aaa gga tat ttt aat tat gat gaa aaa tct 240
Ile Ile Gly Glu Gly His Lys Gly Tyr Phe Asn Tyr Asp Glu Lys Ser
      65             70             75             80

aaa gat cca aaa tct cct ttg aat cct tgg gct ttt ata cga gta aaa 288
Lys Asp Pro Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val Lys
      85             90             95

aat gaa gct att acc tta aaa gct tct ctt gaa agc ata ttg cct gct 336
Asn Glu Ala Ile Thr Leu Lys Ala Ser Leu Glu Ser Ile Leu Pro Ala
      100            105            110

atc caa aga ggt gtt ata gga tat aat gat tgt acc gat gga agt gaa 384
Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser Glu
      115            120            125

gaa ata att cta gaa ttt tgc aaa caa tat cct tca ttt ata cca ata 432
Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro Ile
      130            135            140

aaa tat cct tat gaa att caa att caa aac cca aaa tca gaa gaa aat 480
Lys Tyr Pro Tyr Glu Ile Gln Ile Gln Asn Pro Lys Ser Glu Glu Asn
      145            150            155            160

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aaa ctc tat agc tat tat aat tat gtt gca agt ttt ata cca aaa gat	528
Lys Leu Tyr Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Lys Asp	
165 170 175	
gag tgg ctt ata aaa ata gat gtg gat cat atc tat gat gct aaa aaa	576
Glu Trp Leu Ile Lys Ile Asp Val Asp His Ile Tyr Asp Ala Lys Lys	
180 185 190	
ctt tat aaa agc ttc tat ata cca aaa aac aaa tat gat gta gtt agt	624
Leu Tyr Lys Ser Phe Tyr Ile Pro Lys Asn Lys Tyr Asp Val Val Ser	
195 200 205	
tat tca agg gtt gat att cac tat ttt aat gat aat ttt ttt ctt tgt	672
Tyr Ser Arg Val Asp Ile His Tyr Phe Asn Asp Asn Phe Phe Leu Cys	
210 215 220	
aaa gat aat aat ggc aat ata ttg aaa gaa cca gga gat tgc ttg ctt	720
Lys Asp Asn Asn Gly Asn Ile Leu Lys Glu Pro Gly Asp Cys Leu Leu	
225 230 235 240	
atc aat aat tat aac tta aaa tgg aaa gaa gta tta att gac aga atc	768
Ile Asn Asn Tyr Asn Leu Lys Trp Lys Glu Val Leu Ile Asp Arg Ile	
245 250 255	
aat aac aat tgg aaa aaa gca aca aaa caa agt ttt tct tca aat ata	816
Asn Asn Asn Trp Lys Lys Ala Thr Lys Gln Ser Phe Ser Ser Asn Ile	
260 265 270	
cac tct tta gag caa tta aag tat aaa cac agg ata tta ttt cac act	864
His Ser Leu Glu Gln Leu Lys Tyr Lys His Arg Ile Leu Phe His Thr	
275 280 285	
gaa tta aat aat tat cat ttt cct ttt tta aaa aaa cat aga gct caa	912
Glu Leu Asn Asn Tyr His Phe Pro Phe Leu Lys Lys His Arg Ala Gln	
290 295 300	
gat att tat aaa tat aat tgg ata agt att gaa gaa ttt aaa aaa ttc	960
Asp Ile Tyr Lys Tyr Asn Trp Ile Ser Ile Glu Glu Phe Lys Lys Phe	
305 310 315 320	
tat tta caa aat att aat cat aaa ata gaa cct tct atg att tca aaa	1008
Tyr Leu Gln Asn Ile Asn His Lys Ile Glu Pro Ser Met Ile Ser Lys	
325 330 335	
gaa act cta aaa aaa ata ttc tta aca ttg ttt taa	1044
Glu Thr Leu Lys Lys Ile Phe Leu Thr Leu Phe	
340 345	

<210> 17

<211> 347

<212> PRT

<213> Campylobacter jejuni

<220>

<223> beta-1,4 N-acetylgalactosaminyl (GalNAc)  
transferase from C. jejuni strain OH4384 (ORF 5a  
of lipooligosaccharide (LOS) biosynthesis locus)

<400> 17

Met Leu Phe Gln Ser Tyr Phe Val Lys Ile Ile Cys Leu Phe Ile Pro  
1 5 10 15  
Phe Arg Lys Ile Arg His Lys Ile Lys Lys Thr Phe Leu Leu Lys Asn  
20 25 30  
Ile Gln Arg Asp Lys Ile Asp Ser Tyr Leu Pro Lys Lys Thr Leu Val  
35 40 45  
Gln Ile Asn Lys Tyr Asn Asn Glu Asp Leu Ile Lys Leu Asn Lys Ala  
50 55 60  
Ile Ile Gly Glu Gly His Lys Gly Tyr Phe Asn Tyr Asp Glu Lys Ser  
65 70 75 80  
Lys Asp Pro Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val Lys  
85 90 95  
Asn Glu Ala Ile Thr Leu Lys Ala Ser Leu Glu Ser Ile Leu Pro Ala  
100 105 110  
Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser Glu  
115 120 125  
Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro Ile  
130 135 140  
Lys Tyr Pro Tyr Glu Ile Gln Ile Gln Asn Pro Lys Ser Glu Glu Asn  
145 150 155 160  
Lys Leu Tyr Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Lys Asp  
165 170 175  
Glu Trp Leu Ile Lys Ile Asp Val Asp His Ile Tyr Asp Ala Lys Lys  
180 185 190  
Leu Tyr Lys Ser Phe Tyr Ile Pro Lys Asn Lys Tyr Asp Val Val Ser  
195 200 205  
Tyr Ser Arg Val Asp Ile His Tyr Phe Asn Asp Asn Phe Phe Leu Cys  
210 215 220  
Lys Asp Asn Asn Gly Asn Ile Leu Lys Glu Pro Gly Asp Cys Leu Leu  
225 230 235 240  
Ile Asn Asn Tyr Asn Leu Lys Trp Lys Glu Val Leu Ile Asp Arg Ile  
245 250 255  
Asn Asn Asn Trp Lys Lys Ala Thr Lys Gln Ser Phe Ser Ser Asn Ile  
260 265 270  
His Ser Leu Glu Gln Leu Lys Tyr Lys His Arg Ile Leu Phe His Thr  
275 280 285  
Glu Leu Asn Asn Tyr His Phe Pro Phe Leu Lys Lys His Arg Ala Gln  
290 295 300  
Asp Ile Tyr Lys Tyr Asn Trp Ile Ser Ile Glu Glu Phe Lys Lys Phe  
305 310 315 320  
Tyr Leu Gln Asn Ile Asn His Lys Ile Glu Pro Ser Met Ile Ser Lys  
325 330 335  
Glu Thr Leu Lys Lys Ile Phe Leu Thr Leu Phe  
340 345

<210> 18

<211> 1608

<212> DNA

<213> Campylobacter jejuni

<220>

<221> CDS

<222> (1)..(1608)

<223> beta-1,4 N-acetylgalactosaminyl (GalNAc)  
transferase from C. jejuni O:1

<400> 18

atg act ttg ttt tat aaa att ata gct ttt tta aga ttg ctt aaa att	48
Met Thr Leu Phe Tyr Lys Ile Ile Ala Phe Leu Arg Leu Leu Lys Ile	
1 5 10 15	
gat aaa aaa tta aaa ttt gat aat gaa tat ttt tta aac tta aat aaa	96
Asp Lys Lys Leu Lys Phe Asp Asn Glu Tyr Phe Leu Asn Leu Asn Lys	
20 25 30	
aaa atc tac aat gaa aag cat aaa ggt ttt ttt gat ttt gat cca aac	144
Lys Ile Tyr Asn Glu Lys His Lys Gly Phe Phe Asp Phe Asp Pro Asn	
35 40 45	
tca aaa gat aca aaa tct cct tta aat cca tgg gct ttt ata aga gta	192
Ser Lys Asp Thr Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val	
50 55 60	
aaa aat gaa gcc act act tta aga gta tca ctt gaa agt atg tta cct	240
Lys Asn Glu Ala Thr Thr Leu Arg Val Ser Leu Glu Ser Met Leu Pro	
65 70 75 80	
gcc ata caa aga ggt gtt ata gga tat aat gat tgt act gat gga agt	288
Ala Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser	
85 90 95	
gaa gaa att att ttg gaa ttt tgc aaa caa tac cct tcg ttt ata cca	336
Glu Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro	
100 105 110	
gta aaa tat ccc cat gag gtg caa att gaa aat ccg caa agc gaa gaa	384
Val Lys Tyr Pro His Glu Val Gln Ile Glu Asn Pro Gln Ser Glu Glu	
115 120 125	
aat aaa ctt cat agt tat tat aac tat gta gct agt ttt ata ccg caa	432
Asn Lys Leu His Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Gln	
130 135 140	
gat gag tgg ctt ata aaa ata gat gtg gat cat tac tat gat gca aaa	480
Asp Glu Trp Leu Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys	
145 150 155 160	
aaa tta tat aag agt ttt tat atg gca tca aaa aat act gct gtt aga	528
Lys Leu Tyr Lys Ser Phe Tyr Met Ala Ser Lys Asn Thr Ala Val Arg	
165 170 175	
ttt cca aga att aat ttt tta ata cta gat aaa att gta att caa aat	576
Phe Pro Arg Ile Asn Phe Leu Ile Leu Asp Lys Ile Val Ile Gln Asn	
180 185 190	
ata gga gaa tgt ggt ttt atc gat gga ggg gat caa ttg tta att caa	624
Ile Gly Glu Cys Gly Phe Ile Asp Gly Gly Asp Gln Leu Leu Ile Gln	
195 200 205	
aag tgc aat agt gta ttt ata gaa aga atg gtt tca aag caa agt cag	672
Lys Cys Asn Ser Val Phe Ile Glu Arg Met Val Ser Lys Gln Ser Gln	
210 215 220	
tgg att gat cct gaa aaa act gtg aaa gaa ttg tat tct gaa cag caa	720
Trp Ile Asp Pro Glu Lys Thr Val Lys Glu Leu Tyr Ser Glu Gln Gln	
225 230 235 240	

att ata ccc aaa cat ata aaa atc tta caa gca gaa tta ctt caa tgg	768
Ile Ile Pro Lys His Ile Lys Ile Leu Gln Ala Glu Leu Leu Gln Trp	
245 250 255	
cat ttt cct gct tta aaa tat cat aga aat gat tat caa aaa cat ttg	816
His Phe Pro Ala Leu Lys Tyr His Arg Asn Asp Tyr Gln Lys His Leu	
260 265 270	
gat gct tta act tta gaa gat ttt aaa aaa atc cat tat aga cat aga	864
Asp Ala Leu Thr Leu Glu Asp Phe Lys Lys Ile His Tyr Arg His Arg	
275 280 285	
aaa ata aag aaa ata aat tat aca atg ctt gat gaa aaa gta att cgt	912
Lys Ile Lys Lys Ile Asn Tyr Thr Met Leu Asp Glu Lys Val Ile Arg	
290 295 300	
gaa ata tta gat aaa ttt aaa ttg agt ggt aaa aaa atg act tta gct	960
Glu Ile Leu Asp Lys Phe Lys Leu Ser Gly Lys Lys Met Thr Leu Ala	
305 310 315 320	
ata ata cct gct cga gct ggt tca aaa ggt ata aaa aat aaa aat tta	1008
Ile Ile Pro Ala Arg Ala Gly Ser Lys Gly Ile Lys Asn Lys Asn Leu	
325 330 335	
gct ctt ttg cat gat agg cct ttg ttg tat tat act atc aat gca gca	1056
Ala Leu Leu His Asp Arg Pro Leu Leu Tyr Tyr Thr Ile Asn Ala Ala	
340 345 350	
aaa aat tca aag tat gta gat aaa att gtt tta agt agt gat ggc gat	1104
Lys Asn Ser Lys Tyr Val Asp Lys Ile Val Leu Ser Ser Asp Gly Asp	
355 360 365	
gat ata tta gaa tat gga caa act caa ggt gta gat gtg tta aaa aga	1152
Asp Ile Leu Glu Tyr Gly Gln Thr Gln Gly Val Asp Val Leu Lys Arg	
370 375 380	
cct aaa gaa tta gcg cta gat gat aca act agt gat aag gtt gta ttg	1200
Pro Lys Glu Leu Ala Leu Asp Asp Thr Thr Ser Asp Lys Val Val Leu	
385 390 395 400	
cat acc ttg agt ttt tat aaa gat tat gaa aat att gtt tta tta caa	1248
His Thr Leu Ser Phe Tyr Lys Asp Tyr Glu Asn Ile Val Leu Leu Gln	
405 410 415	
ccc act tct cct tta agg aca aat gta cat ata gat gaa gct ttt tta	1296
Pro Thr Ser Pro Leu Arg Thr Asn Val His Ile Asp Glu Ala Phe Leu	
420 425 430	
aaa ttt aaa aat gaa aac tca aat gca tta ata agt gtt gta gaa tgt	1344
Lys Phe Lys Asn Glu Asn Ser Asn Ala Leu Ile Ser Val Val Glu Cys	
435 440 445	
gat aat aaa att tta aaa gct ttt ata gat gat aat ggt aac tta aaa	1392
Asp Asn Lys Ile Leu Lys Ala Phe Ile Asp Asp Asn Gly Asn Leu Lys	
450 455 460	
gga att tgt gat aac aaa tat cca ttt atg cct aga caa aaa tta cca	1440
Gly Ile Cys Asp Asn Lys Tyr Pro Phe Met Pro Arg Gln Lys Leu Pro	
465 470 475 480	



aaa act tat atg agt aat ggt gca att tat ata gta aag tca aat tta 1488  
 Lys Thr Tyr Met Ser Asn Gly Ala Ile Tyr Ile Val Lys Ser Asn Leu  
                     485                    490                    495

ttt tta aat aac cca act ttt cta caa gaa aaa aca agt tgc tat ata 1536  
 Phe Leu Asn Asn Pro Thr Phe Leu Gln Glu Lys Thr Ser Cys Tyr Ile  
                     500                    505                    510

atg gac gaa aaa gct agt ttg gat ata gat aca aca gag gat tta aaa 1584  
 Met Asp Glu Lys Ala Ser Leu Asp Ile Asp Thr Thr Glu Asp Leu Lys  
                     515                    520                    525

aga gtt aat aat ata agc ttc tta 1608  
 Arg Val Asn Asn Ile Ser Phe Leu  
                     530                    535

<210> 19

<211> 536

<212> PRT

<213> Campylobacter jejuni

<223> beta-1,4 N-acetylgalactosaminyl (GalNAc)  
 transferase from C. jejuni O:1

<400> 19

Met Thr Leu Phe Tyr Lys Ile Ile Ala Phe Leu Arg Leu Leu Lys Ile  
 1                    5                    10                    15  
 Asp Lys Lys Leu Lys Phe Asp Asn Glu Tyr Phe Leu Asn Leu Asn Lys  
                     20                    25                    30  
 Lys Ile Tyr Asn Glu Lys His Lys Gly Phe Phe Asp Phe Asp Pro Asn  
                     35                    40                    45  
 Ser Lys Asp Thr Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val  
                     50                    55                    60  
 Lys Asn Glu Ala Thr Thr Leu Arg Val Ser Leu Glu Ser Met Leu Pro  
                     65                    70                    75                    80  
 Ala Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser  
                     85                    90                    95  
 Glu Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro  
                     100                    105                    110  
 Val Lys Tyr Pro His Glu Val Gln Ile Glu Asn Pro Gln Ser Glu Glu  
                     115                    120                    125  
 Asn Lys Leu His Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Gln  
                     130                    135                    140  
 Asp Glu Trp Leu Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys  
                     145                    150                    155                    160  
 Lys Leu Tyr Lys Ser Phe Tyr Met Ala Ser Lys Asn Thr Ala Val Arg  
                     165                    170                    175  
 Phe Pro Arg Ile Asn Phe Leu Ile Leu Asp Lys Ile Val Ile Gln Asn  
                     180                    185                    190  
 Ile Gly Glu Cys Gly Phe Ile Asp Gly Gly Asp Gln Leu Leu Ile Gln  
                     195                    200                    205  
 Lys Cys Asn Ser Val Phe Ile Glu Arg Met Val Ser Lys Gln Ser Gln  
                     210                    215                    220  
 Trp Ile Asp Pro Glu Lys Thr Val Lys Glu Leu Tyr Ser Glu Gln Gln  
                     225                    230                    235                    240  
 Ile Ile Pro Lys His Ile Lys Ile Leu Gln Ala Glu Leu Leu Gln Trp  
                     245                    250                    255  
 His Phe Pro Ala Leu Lys Tyr His Arg Asn Asp Tyr Gln Lys His Leu  
                     260                    265                    270

Asp Ala Leu Thr Leu Glu Asp Phe Lys Lys Ile His Tyr Arg His Arg  
 275 280 285  
 Lys Ile Lys Lys Ile Asn Tyr Thr Met Leu Asp Glu Lys Val Ile Arg  
 290 295 300  
 Glu Ile Leu Asp Lys Phe Lys Leu Ser Gly Lys Lys Met Thr Leu Ala  
 305 310 315 320  
 Ile Ile Pro Ala Arg Ala Gly Ser Lys Gly Ile Lys Asn Lys Asn Leu  
 325 330 335  
 Ala Leu Leu His Asp Arg Pro Leu Leu Tyr Tyr Thr Ile Asn Ala Ala  
 340 345 350  
 Lys Asn Ser Lys Tyr Val Asp Lys Ile Val Leu Ser Ser Asp Gly Asp  
 355 360 365  
 Asp Ile Leu Glu Tyr Gly Gln Thr Gln Gly Val Asp Val Leu Lys Arg  
 370 375 380  
 Pro Lys Glu Leu Ala Leu Asp Asp Thr Thr Ser Asp Lys Val Val Leu  
 385 390 395 400  
 His Thr Leu Ser Phe Tyr Lys Asp Tyr Glu Asn Ile Val Leu Leu Gln  
 405 410 415  
 Pro Thr Ser Pro Leu Arg Thr Asn Val His Ile Asp Glu Ala Phe Leu  
 420 425 430  
 Lys Phe Lys Asn Glu Asn Ser Asn Ala Leu Ile Ser Val Val Glu Cys  
 435 440 445  
 Asp Asn Lys Ile Leu Lys Ala Phe Ile Asp Asp Asn Gly Asn Leu Lys  
 450 455 460  
 Gly Ile Cys Asp Asn Lys Tyr Pro Phe Met Pro Arg Gln Lys Leu Pro  
 465 470 475 480  
 Lys Thr Tyr Met Ser Asn Gly Ala Ile Tyr Ile Val Lys Ser Asn Leu  
 485 490 495  
 Phe Leu Asn Asn Pro Thr Phe Leu Gln Glu Lys Thr Ser Cys Tyr Ile  
 500 505 510  
 Met Asp Glu Lys Ala Ser Leu Asp Ile Asp Thr Thr Glu Asp Leu Lys  
 515 520 525  
 Arg Val Asn Asn Ile Ser Phe Leu  
 530 535

<210> 20

<211> 1056

<212> DNA

<213> Campylobacter jejuni

<220>

<221> CDS

<222> (1)..(1056)

<223> beta-1,4 N-acetylgalactosaminyl (GalNAc)  
transferase from C. jejuni O:10

<400> 20

atg cta ttt caa tca tac ttt gtg aaa ata att tgc tta ttc atc cct 48  
 Met Leu Phe Gln Ser Tyr Phe Val Lys Ile Ile Cys Leu Phe Ile Pro  
 1 5 10 15

ttt aga aaa att aga cat aaa ata aaa aca ttt tta cta aaa aac 96  
 Phe Arg Lys Ile Arg His Lys Ile Lys Lys Thr Phe Leu Leu Lys Asn  
 20 25 30

ata caa cga gat aaa atc gat tct tat cta cca aaa aaa act ctt ata 144  
 Ile Gln Arg Asp Lys Ile Asp Ser Tyr Leu Pro Lys Lys Thr Leu Ile  
 35 40 45

caa att aat aaa tac aac aat gaa gat tta att aaa ctt aat aaa gct	192
Gln Ile Asn Lys Tyr Asn Asn Glu Asp Leu Ile Lys Leu Asn Lys Ala	
50 55 60	
att ata ggg ggg ggg cat aaa gga tat ttt aat tat gat gaa aaa tct	240
Ile Ile Gly Gly Gly His Lys Gly Tyr Phe Asn Tyr Asp Glu Lys Ser	
65 70 75 80	
aaa gat cca aaa tct cct ttg aat cct tgg gct ttt ata cga gta aaa	288
Lys Asp Pro Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val Lys	
85 90 95	
aat gaa gct att acc tta aaa gct tct ctt gaa agc ata ttg cct gct	336
Asn Glu Ala Ile Thr Leu Lys Ala Ser Leu Glu Ser Ile Leu Pro Ala	
100 105 110	
att caa aga ggt gtt ata gga tat aat gat tgc acc gat gga agt gaa	384
Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser Glu	
115 120 125	
gaa ata att cta gaa ttt tgc aaa caa tat cct tca ttt ata cca ata	432
Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro Ile	
130 135 140	
aaa tat cct tat gaa att caa att caa aac cca aaa tca gaa gaa aat	480
Lys Tyr Pro Tyr Glu Ile Gln Ile Gln Asn Pro Lys Ser Glu Glu Asn	
145 150 155 160	
aaa ctc tat agc tat tat aat tat gtt gca agt ttt ata cca aaa gat	528
Lys Leu Tyr Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Lys Asp	
165 170 175	
gag tgg ctc ata aaa ata gat gtg gat cat tat tat gat gca aaa aaa	576
Glu Trp Leu Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys Lys	
180 185 190	
tta tat aag agt ttt tat ata cct aga aaa aat tat cat gta att agt	624
Leu Tyr Lys Ser Phe Tyr Ile Pro Arg Lys Asn Tyr His Val Ile Ser	
195 200 205	
tac tct agg ata gat ttt ata ttt aat gaa gaa aaa ttt tat gtt tat	672
Tyr Ser Arg Ile Asp Phe Ile Phe Asn Glu Glu Lys Phe Tyr Val Tyr	
210 215 220	
cgg aat aag gag ggg gag att tta aaa gct cct gga gat tgt tta gca	720
Arg Asn Lys Glu Gly Glu Ile Leu Lys Ala Pro Gly Asp Cys Leu Ala	
225 230 235 240	
ata caa aac act aac tta ttt tgg aaa gaa ata ctt att gaa gat gat	768
Ile Gln Asn Thr Asn Leu Phe Trp Lys Glu Ile Leu Ile Glu Asp Asp	
245 250 255	
aca ttt aag tgg aat act gca aaa aat aat ata gag aat gca aaa tca	816
Thr Phe Lys Trp Asn Thr Ala Lys Asn Asn Ile Glu Asn Ala Lys Ser	
260 265 270	
tat gaa att tta aaa gtt aga aat aga att tat ttt act aca gaa ctt	864
Tyr Glu Ile Leu Lys Val Arg Asn Arg Ile Tyr Phe Thr Thr Glu Leu	
275 280 285	

aat aat tat cat ttt cca ttt ata aaa aat tat aga aaa aat gat tat 912  
 Asn Asn Tyr His Phe Pro Phe Ile Lys Asn Tyr Arg Lys Asn Asp Tyr  
 290 295 300  
 aag cag tta aat tgg gtt agc tta gat gat ttt att aaa aat tat aaa 960  
 Lys Gln Leu Asn Trp Val Ser Leu Asp Asp Phe Ile Lys Asn Tyr Lys  
 305 310 315 320  
 gaa aaa tta aaa aat caa ata gat ttt aaa atg cta gaa tac aaa aca 1008  
 Glu Lys Leu Lys Asn Gln Ile Asp Phe Lys Met Leu Glu Tyr Lys Thr  
 325 330 335  
 tta aaa aaa gtg tac aaa aag ctt aca tct tca gca agc gat aaa att 1056  
 Leu Lys Lys Val Tyr Lys Lys Leu Thr Ser Ser Ala Ser Asp Lys Ile  
 340 345 350

<210> 21  
 <211> 352  
 <212> PRT  
 <213> Campylobacter jejuni

<220>  
 <223> beta-1,4 N-acetylgalactosaminyl (GalNAc)  
 transferase from C. jejuni O:10

<400> 21  
 Met Leu Phe Gln Ser Tyr Phe Val Lys Ile Ile Cys Leu Phe Ile Pro  
 1 5 10 15  
 Phe Arg Lys Ile Arg His Lys Ile Lys Thr Phe Leu Leu Lys Asn  
 20 25 30  
 Ile Gln Arg Asp Lys Ile Asp Ser Tyr Leu Pro Lys Lys Thr Leu Ile  
 35 40 45  
 Gln Ile Asn Lys Tyr Asn Asn Glu Asp Leu Ile Lys Leu Asn Lys Ala  
 50 55 60  
 Ile Ile Gly Gly Gly His Lys Gly Tyr Phe Asn Tyr Asp Glu Lys Ser  
 65 70 75 80  
 Lys Asp Pro Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val Lys  
 85 90 95  
 Asn Glu Ala Ile Thr Leu Lys Ala Ser Leu Glu Ser Ile Leu Pro Ala  
 100 105 110  
 Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser Glu  
 115 120 125  
 Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro Ile  
 130 135 140  
 Lys Tyr Pro Tyr Glu Ile Gln Ile Gln Asn Pro Lys Ser Glu Glu Asn  
 145 150 155 160  
 Lys Leu Tyr Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Lys Asp  
 165 170 175  
 Glu Trp Leu Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys Lys  
 180 185 190  
 Leu Tyr Lys Ser Phe Tyr Ile Pro Arg Lys Asn Tyr His Val Ile Ser  
 195 200 205  
 Tyr Ser Arg Ile Asp Phe Ile Phe Asn Glu Glu Lys Phe Tyr Val Tyr  
 210 215 220  
 Arg Asn Lys Glu Gly Glu Ile Leu Lys Ala Pro Gly Asp Cys Leu Ala  
 225 230 235 240  
 Ile Gln Asn Thr Asn Leu Phe Trp Lys Glu Ile Leu Ile Glu Asp Asp  
 245 250 255  
 Thr Phe Lys Trp Asn Thr Ala Lys Asn Asn Ile Glu Asn Ala Lys Ser  
 260 265 270

Tyr Glu Ile Leu Lys Val Arg Asn Arg Ile Tyr Phe Thr Thr Glu Leu  
           275                          280                          285  
 Asn Asn Tyr His Phe Pro Phe Ile Lys Asn Tyr Arg Lys Asn Asp Tyr  
           290                          295                          300  
 Lys Gln Leu Asn Trp Val Ser Leu Asp Asp Phe Ile Lys Asn Tyr Lys  
 305                          310                          315                          320  
 Glu Lys Leu Lys Asn Gln Ile Asp Phe Lys Met Leu Glu Tyr Lys Thr  
                           325                          330                          335  
 Leu Lys Lys Val Tyr Lys Lys Leu Thr Ser Ser Ala Ser Asp Lys Ile  
                           340                          345                          350

<210> 22  
 <211> 945  
 <212> DNA  
 <213> Campylobacter jejuni

<220>  
 <221> CDS  
 <222> (1)..(945)  
 <223> beta-1,4 N-acetylgalactosaminyl (GalNAc)  
           transferase from C. jejuni O:36

<400> 22  
 atg ctt aaa aaa atc att tct tta tat aaa aga tac tcg att tct aaa 48  
 Met Leu Lys Lys Ile Ile Ser Leu Tyr Lys Arg Tyr Ser Ile Ser Lys  
   1                          5                          10                          15  
  
 aaa ttg gtt tta gat aat gag cat ttc att aag gaa aat aaa aac atc 96  
 Lys Leu Val Leu Asp Asn Glu His Phe Ile Lys Glu Asn Lys Asn Ile  
                           20                          25                          30  
  
 tat gga aaa aaa cat aag ggc ttt ttt gac ttt gat gaa aag gct aag 144  
 Tyr Gly Lys Lys His Lys Gly Phe Phe Asp Phe Asp Glu Lys Ala Lys  
                           35                          40                          45  
  
 gat gtg aaa tca ccc ctt aat cct tgg gga ttt atc agg gtt aaa aat 192  
 Asp Val Lys Ser Pro Leu Asn Pro Trp Gly Phe Ile Arg Val Lys Asn  
   50                          55                          60  
  
 gaa gct tta acc cta aga gtt tct tta gaa agt ata cta cct gct tta 240  
 Glu Ala Leu Thr Leu Arg Val Ser Leu Glu Ser Ile Leu Pro Ala Leu  
   65                          70                          75                          80  
  
 caa aga gga att ata gct tac aac gac tgt gat gat ggg agt gaa gag 288  
 Gln Arg Gly Ile Ile Ala Tyr Asn Asp Cys Asp Asp Gly Ser Glu Glu  
                           85                          90                          95  
  
 ctt att tta gaa ttt tgc aag caa tat ccc aac ttc att gct aaa aaa 336  
 Leu Ile Leu Glu Phe Cys Lys Gln Tyr Pro Asn Phe Ile Ala Lys Lys  
                           100                          105                          110  
  
 tat cct tat aaa gta gat cta gaa aat cct aaa aat gaa gaa aat aaa 384  
 Tyr Pro Tyr Lys Val Asp Leu Glu Asn Pro Lys Asn Glu Glu Asn Lys  
                           115                          120                          125  
  
 ctt tac tct tat tac aat tgg gca gca tct ttt ata ccc tta gat gag 432  
 Leu Tyr Ser Tyr Tyr Asn Trp Ala Ala Ser Phe Ile Pro Leu Asp Glu  
   130                          135                          140

tgg ttt ata aaa atc gat gtg gat cat tac tac gat gcc aag aag ctt	480
Trp Phe Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys Lys Leu	
145 150 155 160	
tat aag agt ttt tat agg att gat caa gaa aat aaa gcc tta tgc tac	528
Tyr Lys Ser Phe Tyr Arg Ile Asp Gln Glu Asn Lys Ala Leu Cys Tyr	
165 170 175	
cca aga att aat ttt ata atc tta aat gga aat att tat gtg caa aat	576
Pro Arg Ile Asn Phe Ile Ile Leu Asn Gly Asn Ile Tyr Val Gln Asn	
180 185 190	
agt gga aat tat gga ttc ata ggg ggg ggg gat caa ctc ttg att aaa	624
Ser Gly Asn Tyr Gly Phe Ile Gly Gly Gly Asp Gln Leu Leu Ile Lys	
195 200 205	
aga aga aat agt agc ttt ata gaa aga agg gtt tca aaa aaa agc caa	672
Arg Arg Asn Ser Ser Phe Ile Glu Arg Arg Val Ser Lys Lys Ser Gln	
210 215 220	
tgg ata gat cct aag gga ctt ata gaa gaa ctc tac tcc gag caa caa	720
Trp Ile Asp Pro Lys Gly Leu Ile Glu Glu Leu Tyr Ser Glu Gln Gln	
225 230 235 240	
gtc tta tct caa gga gtg aaa ata cta caa gct ccc cta ctt cag tgg	768
Val Leu Ser Gln Gly Val Lys Ile Leu Gln Ala Pro Leu Leu Gln Trp	
245 250 255	
cat ttt cct gcc tta aaa tac cgc cga aac gat tac caa caa tat tta	816
His Phe Pro Ala Leu Lys Tyr Arg Arg Asn Asp Tyr Gln Gln Tyr Leu	
260 265 270	
gat atc ttg agt tta gaa gaa ttt cag gcc ttt cat cgt aag agc aaa	864
Asp Ile Leu Ser Leu Glu Glu Phe Gln Ala Phe His Arg Lys Ser Lys	
275 280 285	
gag gct aaa aaa ata gac ttt gcc atg cta aaa cgc cct gta atc gag	912
Glu Ala Lys Lys Ile Asp Phe Ala Met Leu Lys Arg Pro Val Ile Glu	
290 295 300	
caa ata tta aag aaa ttt caa gga gag ata aaa	945
Gln Ile Leu Lys Lys Phe Gln Gly Glu Ile Lys	
305 310 315	

<210> 23

<211> 315

<212> PRT

<213> Campylobacter jejuni

<220>

<223> beta-1,4 N-acetylgalactosaminyl (GalNAc)  
transferase from C. jejuni O:36

<400> 23

Met	Leu	Lys	Lys	Ile	Ile	Ser	Leu	Tyr	Lys	Arg	Tyr	Ser	Ile	Ser	Lys
1				5					10				15		

Lys	Leu	Val	Leu	Asp	Asn	Glu	His	Phe	Ile	Lys	Glu	Asn	Lys	Asn	Ile
			20					25					30		

Tyr	Gly	Lys	Lys	His	Lys	Gly	Phe	Phe	Asp	Phe	Asp	Glu	Lys	Ala	Lys
		35				40						45			

Asp Val Lys Ser Pro Leu Asn Pro Trp Gly Phe Ile Arg Val Lys Asn  
 50 55 60  
 Glu Ala Leu Thr Leu Arg Val Ser Leu Glu Ser Ile Leu Pro Ala Leu  
 65 70 75 80  
 Gln Arg Gly Ile Ile Ala Tyr Asn Asp Cys Asp Asp Gly Ser Glu Glu  
 85 90 95  
 Leu Ile Leu Glu Phe Cys Lys Gln Tyr Pro Asn Phe Ile Ala Lys Lys  
 100 105 110  
 Tyr Pro Tyr Lys Val Asp Leu Glu Asn Pro Lys Asn Glu Glu Asn Lys  
 115 120 125  
 Leu Tyr Ser Tyr Tyr Asn Trp Ala Ala Ser Phe Ile Pro Leu Asp Glu  
 130 135 140  
 Trp Phe Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys Lys Leu  
 145 150 155 160  
 Tyr Lys Ser Phe Tyr Arg Ile Asp Gln Glu Asn Lys Ala Leu Cys Tyr  
 165 170 175  
 Pro Arg Ile Asn Phe Ile Ile Leu Asn Gly Asn Ile Tyr Val Gln Asn  
 180 185 190  
 Ser Gly Asn Tyr Gly Phe Ile Gly Gly Gly Asp Gln Leu Leu Ile Lys  
 195 200 205  
 Arg Arg Asn Ser Ser Phe Ile Glu Arg Arg Val Ser Lys Lys Ser Gln  
 210 215 220  
 Trp Ile Asp Pro Lys Gly Leu Ile Glu Glu Leu Tyr Ser Glu Gln Gln  
 225 230 235 240  
 Val Leu Ser Gln Gly Val Lys Ile Leu Gln Ala Pro Leu Leu Gln Trp  
 245 250 255  
 His Phe Pro Ala Leu Lys Tyr Arg Arg Asn Asp Tyr Gln Gln Tyr Leu  
 260 265 270  
 Asp Ile Leu Ser Leu Glu Glu Phe Gln Ala Phe His Arg Lys Ser Lys  
 275 280 285  
 Glu Ala Lys Lys Ile Asp Phe Ala Met Leu Lys Arg Pro Val Ile Glu  
 290 295 300  
 Gln Ile Leu Lys Lys Phe Gln Gly Glu Ile Lys  
 305 310 315

<210> 24  
 <211> 1608  
 <212> DNA  
 <213> Campylobacter jejuni

<220>  
 <221> CDS  
 <222> (1)..(1608)  
 <223> beta-1,4 N-acetylgalactosaminyl (GalNAc)  
 transferase from C. jejuni NCTC 11168

<400> 24  
 atg act ttg ttt tat aaa att ata gct ttt tta aga ttg ctt aaa att 48  
 Met Thr Leu Phe Tyr Lys Ile Ile Ala Phe Leu Arg Leu Leu Lys Ile  
 1 5 10 15  
 gat aaa aaa tta aaa ttt gat aat gaa tat ttt tta aac tta aat aaa 96  
 Asp Lys Lys Leu Lys Phe Asp Asn Glu Tyr Phe Leu Asn Leu Asn Lys  
 20 25 30  
 aaa atc tac gat gaa aag cat aaa ggt ttt ttt gat ttt gat cca aac 144  
 Lys Ile Tyr Asp Glu Lys His Lys Gly Phe Phe Asp Phe Asp Pro Asn  
 35 40 45

tca aaa gat aca aaa tct cct tta aat cca tgg gct ttt ata aga gta	192
Ser Lys Asp Thr Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val	
50 55 60	
aaa aat gaa gcc act act tta aga gta tca ctt gaa agt atg tta cct	240
Lys Asn Glu Ala Thr Thr Leu Arg Val Ser Leu Glu Ser Met Leu Pro	
65 70 75 80	
gcc ata caa aga ggt gtt ata gga tat aat gat tgt act gat gga agt	288
Ala Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser	
85 90 95	
gaa gaa att att ttg gaa ttt tgc aaa caa tac cct tcg ttt ata cca	336
Glu Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro	
100 105 110	
gta aaa tat ccc cat gag gtg caa att gaa aat ccg caa agc gaa gaa	384
Val Lys Tyr Pro His Glu Val Gln Ile Glu Asn Pro Gln Ser Glu Glu	
115 120 125	
aat aaa ctt cat agt tat tat aac tat gta gct agt ttt ata ccg caa	432
Asn Lys Leu His Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Gln	
130 135 140	
gat gag tgg ctt ata aaa ata gat gtg gat cat tac tat gat gca aaa	480
Asp Glu Trp Leu Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys	
145 150 155 160	
aaa tta tat aag agt ttt tat atg gca tca aaa aat act gct gtt aga	528
Lys Leu Tyr Lys Ser Phe Tyr Met Ala Ser Lys Asn Thr Ala Val Arg	
165 170 175	
ttt cca aga att aat ttt tta ata cta gat aaa att gta att caa aat	576
Phe Pro Arg Ile Asn Phe Leu Ile Leu Asp Lys Ile Val Ile Gln Asn	
180 185 190	
ata gga gaa tgt ggt ttt atc gat gga ggg gat caa ttg tta att caa	624
Ile Gly Glu Cys Gly Phe Ile Asp Gly Gly Asp Gln Leu Leu Ile Gln	
195 200 205	
aag tgc aat agt gta ttt ata gaa aga atg gtt tca aag caa agt cag	672
Lys Cys Asn Ser Val Phe Ile Glu Arg Met Val Ser Lys Gln Ser Gln	
210 215 220	
tgg att gat cct gaa aaa act gtg aaa gaa ttg tat tct gaa cag caa	720
Trp Ile Asp Pro Glu Lys Thr Val Lys Glu Leu Tyr Ser Glu Gln Gln	
225 230 235 240	
att ata ccc aaa cat ata aaa atc tta caa gca gaa tta ctt caa tgg	768
Ile Ile Pro Lys His Ile Lys Ile Leu Gln Ala Glu Leu Leu Gln Trp	
245 250 255	
cat ttt cct gct tta aaa tat cat aga aat gat tat caa aaa cat ttg	816
His Phe Pro Ala Leu Lys Tyr His Arg Asn Asp Tyr Gln Lys His Leu	
260 265 270	
gat gct tta act tta gaa gat ttt aaa aaa atc cat tat aga cat aga	864
Asp Ala Leu Thr Leu Glu Asp Phe Lys Lys Ile His Tyr Arg His Arg	
275 280 285	



aaa ata aag aaa ata aat tat aca atg ctt gat gaa aaa gta att cgt Lys Ile Lys Lys Ile Asn Tyr Thr Met Leu Asp Glu Lys Val Ile Arg 290 295 300	912
gaa ata tta gat aaa ttt aaa ttg agt ggt aaa aaa atg act tta gct Glu Ile Leu Asp Lys Phe Lys Leu Ser Gly Lys Lys Met Thr Leu Ala 305 310 315 320	960
ata ata cct gct cga gct ggt tca aaa ggt ata aaa aat aaa aat tta Ile Ile Pro Ala Arg Ala Gly Ser Lys Gly Ile Lys Asn Lys Asn Leu 325 330 335	1008
gct ctt ttg cat gat agg cct ttg ttg tat tat act atc aat gca gca Ala Leu Leu His Asp Arg Pro Leu Leu Tyr Tyr Thr Ile Asn Ala Ala 340 345 350	1056
aaa aat tca aag tat gta gat aaa att gtt tta agt agt gat ggc gat Lys Asn Ser Lys Tyr Val Asp Lys Ile Val Leu Ser Ser Asp Gly Asp 355 360 365	1104
gat ata tta gaa tat gga caa act caa ggt gta gat gtg tta aaa aga Asp Ile Leu Glu Tyr Gly Gln Thr Gln Gly Val Asp Val Leu Lys Arg 370 375 380	1152
cct aaa gaa tta gcg cta gat gat aca act agt gat aag gtt gta ttg Pro Lys Glu Leu Ala Leu Asp Asp Thr Thr Ser Asp Lys Val Val Leu 385 390 395 400	1200
cat acc ttg agt ttt tat aaa gat tat gaa aat att gtt tta tta caa His Thr Leu Ser Phe Tyr Lys Asp Tyr Glu Asn Ile Val Leu Leu Gln 405 410 415	1248
ccc act tct cct tta agg aca aat gta cat ata gat gaa gct ttt tta Pro Thr Ser Pro Leu Arg Thr Asn Val His Ile Asp Glu Ala Phe Leu 420 425 430	1296
aaa ttt aaa aat gaa aac tca aat gca tta ata agt gtt gta gaa tgt Lys Phe Lys Asn Glu Asn Ser Asn Ala Leu Ile Ser Val Val Glu Cys 435 440 445	1344
gat aat aaa att tta aaa gct ttt ata gat gat aat ggt aac tta aaa Asp Asn Lys Ile Leu Lys Ala Phe Ile Asp Asp Asn Gly Asn Leu Lys 450 455 460	1392
gga att tgt gat aac aaa tat cca ttt atg cct aga caa aaa tta cca Gly Ile Cys Asp Asn Lys Tyr Pro Phe Met Pro Arg Gln Lys Leu Pro 465 470 475 480	1440
aaa act tat atg agt aat ggt gca att tat ata gta aag tca aat tta Lys Thr Tyr Met Ser Asn Gly Ala Ile Tyr Ile Val Lys Ser Asn Leu 485 490 495	1488
ttt tta aat aac cca act ttt cta caa gaa aaa aca agt tgc tat ata Phe Leu Asn Asn Pro Thr Phe Leu Gln Glu Lys Thr Ser Cys Tyr Ile 500 505 510	1536
atg gac gaa aaa gct agt ttg gat ata gat aca aca gag gat tta aaa Met Asp Glu Lys Ala Ser Leu Asp Ile Asp Thr Thr Glu Asp Leu Lys 515 520 525	1584

aga gtt aat aat ata agc ttc tta  
 Arg Val Asn Asn Ile Ser Phe Leu  
     530                    535

1608

<210> 25  
 <211> 536  
 <212> PRT  
 <213> Campylobacter jejuni

<220>  
 <223> beta-1,4 N-acetylgalactosaminyl (GalNAc)  
       transferase from C. jejuni NCTC 11168

<400> 25  
 Met Thr Leu Phe Tyr Lys Ile Ile Ala Phe Leu Arg Leu Leu Lys Ile  
   1                    5                    10                    15  
 Asp Lys Lys Leu Lys Phe Asp Asn Glu Tyr Phe Leu Asn Leu Asn Lys  
           20                    25                    30  
 Lys Ile Tyr Asp Glu Lys His Lys Gly Phe Phe Asp Phe Asp Pro Asn  
           35                    40                    45  
 Ser Lys Asp Thr Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val  
           50                    55                    60  
 Lys Asn Glu Ala Thr Thr Leu Arg Val Ser Leu Glu Ser Met Leu Pro  
           65                    70                    75                    80  
 Ala Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser  
                     85                    90                    95  
 Glu Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro  
                     100                    105                    110  
 Val Lys Tyr Pro His Glu Val Gln Ile Glu Asn Pro Gln Ser Glu Glu  
           115                    120                    125  
 Asn Lys Leu His Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Gln  
           130                    135                    140  
 Asp Glu Trp Leu Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys  
           145                    150                    155                    160  
 Lys Leu Tyr Lys Ser Phe Tyr Met Ala Ser Lys Asn Thr Ala Val Arg  
                     165                    170                    175  
 Phe Pro Arg Ile Asn Phe Leu Ile Leu Asp Lys Ile Val Ile Gln Asn  
                     180                    185                    190  
 Ile Gly Glu Cys Gly Phe Ile Asp Gly Gly Asp Gln Leu Leu Ile Gln  
           195                    200                    205  
 Lys Cys Asn Ser Val Phe Ile Glu Arg Met Val Ser Lys Gln Ser Gln  
           210                    215                    220  
 Trp Ile Asp Pro Glu Lys Thr Val Lys Glu Leu Tyr Ser Glu Gln Gln  
           225                    230                    235                    240  
 Ile Ile Pro Lys His Ile Lys Ile Leu Gln Ala Glu Leu Leu Gln Trp  
                     245                    250                    255  
 His Phe Pro Ala Leu Lys Tyr His Arg Asn Asp Tyr Gln Lys His Leu  
                     260                    265                    270  
 Asp Ala Leu Thr Leu Glu Asp Phe Lys Lys Ile His Tyr Arg His Arg  
           275                    280                    285  
 Lys Ile Lys Lys Ile Asn Tyr Thr Met Leu Asp Glu Lys Val Ile Arg  
           290                    295                    300  
 Glu Ile Leu Asp Lys Phe Lys Leu Ser Gly Lys Lys Met Thr Leu Ala  
           305                    310                    315                    320  
 Ile Ile Pro Ala Arg Ala Gly Ser Lys Gly Ile Lys Asn Lys Asn Leu  
                     325                    330                    335  
 Ala Leu Leu His Asp Arg Pro Leu Leu Tyr Tyr Thr Ile Asn Ala Ala  
                     340                    345                    350  
 Lys Asn Ser Lys Tyr Val Asp Lys Ile Val Leu Ser Ser Asp Gly Asp  
           355                    360                    365

Asp Ile Leu Glu Tyr Gly Gln Thr Gln Gly Val Asp Val Leu Lys Arg  
 370 375 380  
 Pro Lys Glu Leu Ala Leu Asp Asp Thr Thr Ser Asp Lys Val Val Leu  
 385 390 395 400  
 His Thr Leu Ser Phe Tyr Lys Asp Tyr Glu Asn Ile Val Leu Leu Gln  
 405 410 415  
 Pro Thr Ser Pro Leu Arg Thr Asn Val His Ile Asp Glu Ala Phe Leu  
 420 425 430  
 Lys Phe Lys Asn Glu Asn Ser Asn Ala Leu Ile Ser Val Val Glu Cys  
 435 440 445  
 Asp Asn Lys Ile Leu Lys Ala Phe Ile Asp Asp Asn Gly Asn Leu Lys  
 450 455 460  
 Gly Ile Cys Asp Asn Lys Tyr Pro Phe Met Pro Arg Gln Lys Leu Pro  
 465 470 475 480  
 Lys Thr Tyr Met Ser Asn Gly Ala Ile Tyr Ile Val Lys Ser Asn Leu  
 485 490 495  
 Phe Leu Asn Asn Pro Thr Phe Leu Gln Glu Lys Thr Ser Cys Tyr Ile  
 500 505 510  
 Met Asp Glu Lys Ala Ser Leu Asp Ile Asp Thr Thr Glu Asp Leu Lys  
 515 520 525  
 Arg Val Asn Asn Ile Ser Phe Leu  
 530 535

<210> 26  
 <211> 906  
 <212> DNA  
 <213> Campylobacter jejuni

<220>  
 <221> CDS  
 <222> (1)..(906)  
 <223> beta-1,3-galactosyltransferase from C. jejuni strain  
 OH4384 (ORF 6a of lipooligosaccharide (LOS)  
 biosynthesis locus)

<400> 26  
 atg ttt aaa att tca atc atc tta cca act tat aat gtg gaa caa tat 48  
 Met Phe Lys Ile Ser Ile Ile Leu Pro Thr Tyr Asn Val Glu Gln Tyr  
 1 5 10 15  
 ata gca agg gca ata gaa agc tgt atc aat cag act ttt aaa gat ata 96  
 Ile Ala Arg Ala Ile Glu Ser Cys Ile Asn Gln Thr Phe Lys Asp Ile  
 20 25 30  
 gaa ata att gta gtt gat gat tgt gga aat gat aat agt ata aat ata 144  
 Glu Ile Ile Val Val Asp Asp Cys Gly Asn Asp Asn Ser Ile Asn Ile  
 35 40 45  
 gcc aaa gaa tac tct aaa aaa gac aaa aga ata aaa ata atc cac aat 192  
 Ala Lys Glu Tyr Ser Lys Lys Asp Lys Arg Ile Lys Ile Ile His Asn  
 50 55 60  
 gaa aaa aac tta ggt ctt tta aga gca aga tat gaa ggt gtg aaa gta 240  
 Glu Lys Asn Leu Gly Leu Leu Arg Ala Arg Tyr Glu Gly Val Lys Val  
 65 70 75 80  
 gca aac tct cct tat ata atg ttt tta gat cct gat gat tat ttg gaa 288  
 Ala Asn Ser Pro Tyr Ile Met Phe Leu Asp Pro Asp Asp Tyr Leu Glu  
 85 90 95

cta aat gct tgt gaa gag tgt ata aaa att tta gat gaa cag gat gaa	336
Leu Asn Ala Cys Glu Glu Cys Ile Lys Ile Leu Asp Glu Gln Asp Glu	
100 105 110	
ggt gat tta gtg ttt ttc aat gct att gtt gaa agt aat gtt att tca	384
Val Asp Leu Val Phe Phe Asn Ala Ile Val Glu Ser Asn Val Ile Ser	
115 120 125	
tat aaa aag ttt gac ttt aat tct ggt ttt tat agc aaa aaa gag ttt	432
Tyr Lys Lys Phe Asp Phe Asn Ser Gly Phe Tyr Ser Lys Lys Glu Phe	
130 135 140	
gta aaa aaa att att gca aag aaa aat tta tat tgg act atg tgg ggg	480
Val Lys Lys Ile Ile Ala Lys Lys Asn Leu Tyr Trp Thr Met Trp Gly	
145 150 155 160	
aaa ctt ata aga aag aaa ttg tat tta gaa gct ttt gcg agt tta aga	528
Lys Leu Ile Arg Lys Lys Leu Tyr Leu Glu Ala Phe Ala Ser Leu Arg	
165 170 175	
ctc gag aaa gat gtt aaa atc aat atg gct gaa gat gta ttg tta tat	576
Leu Glu Lys Asp Val Lys Ile Asn Met Ala Glu Asp Val Leu Leu Tyr	
180 185 190	
tat cca atg tta agt caa gct caa aaa ata gca tat atg aac tgt aat	624
Tyr Pro Met Leu Ser Gln Ala Gln Lys Ile Ala Tyr Met Asn Cys Asn	
195 200 205	
tta tat cat tac gtg cct aat aat aat tca att tgt aat act aag aat	672
Leu Tyr His Tyr Val Pro Asn Asn Asn Ser Ile Cys Asn Thr Lys Asn	
210 215 220	
gaa gtg ctt gtt aaa aat aat att caa gag ttg cag ttg gtt tta aac	720
Glu Val Leu Val Lys Asn Asn Ile Gln Glu Leu Gln Leu Val Leu Asn	
225 230 235 240	
tat tta agg caa aat tat att tta aac aag tat tgt agc gtt ctc tat	768
Tyr Leu Arg Gln Asn Tyr Ile Leu Asn Lys Tyr Cys Ser Val Leu Tyr	
245 250 255	
gtg cta att aaa tat ttg cta tat att caa ata tat aaa ata aaa aga	816
Val Leu Ile Lys Tyr Leu Leu Tyr Ile Gln Ile Tyr Lys Ile Lys Arg	
260 265 270	
aca aaa tta atg gtt aca tta tta gct aaa ata aat att tta act tta	864
Thr Lys Leu Met Val Thr Leu Leu Ala Lys Ile Asn Ile Leu Thr Leu	
275 280 285	
aaa att tta ttt aaa tat aaa aaa ttt tta aaa caa tgt taa	906
Lys Ile Leu Phe Lys Tyr Lys Lys Phe Leu Lys Gln Cys	
290 295 300	

<210> 27

<211> 301

<212> PRT

<213> Campylobacter jejuni

<220>  
 <223> beta-1,3-galactosyltransferase from C. jejuni strain  
 OH4384 (ORF 6a of lipooligosaccharide (LOS)  
 biosynthesis locus)

<400> 27  
 Met Phe Lys Ile Ser Ile Ile Leu Pro Thr Tyr Asn Val Glu Gln Tyr  
 1 5 10 15  
 Ile Ala Arg Ala Ile Glu Ser Cys Ile Asn Gln Thr Phe Lys Asp Ile  
 20 25 30  
 Glu Ile Ile Val Val Asp Asp Cys Gly Asn Asp Asn Ser Ile Asn Ile  
 35 40 45  
 Ala Lys Glu Tyr Ser Lys Lys Asp Lys Arg Ile Lys Ile Ile His Asn  
 50 55 60  
 Glu Lys Asn Leu Gly Leu Leu Arg Ala Arg Tyr Glu Gly Val Lys Val  
 65 70 75 80  
 Ala Asn Ser Pro Tyr Ile Met Phe Leu Asp Pro Asp Asp Tyr Leu Glu  
 85 90 95  
 Leu Asn Ala Cys Glu Glu Cys Ile Lys Ile Leu Asp Glu Gln Asp Glu  
 100 105 110  
 Val Asp Leu Val Phe Phe Asn Ala Ile Val Glu Ser Asn Val Ile Ser  
 115 120 125  
 Tyr Lys Lys Phe Asp Phe Asn Ser Gly Phe Tyr Ser Lys Lys Glu Phe  
 130 135 140  
 Val Lys Lys Ile Ile Ala Lys Lys Asn Leu Tyr Trp Thr Met Trp Gly  
 145 150 155 160  
 Lys Leu Ile Arg Lys Lys Leu Tyr Leu Glu Ala Phe Ala Ser Leu Arg  
 165 170 175  
 Leu Glu Lys Asp Val Lys Ile Asn Met Ala Glu Asp Val Leu Leu Tyr  
 180 185 190  
 Tyr Pro Met Leu Ser Gln Ala Gln Lys Ile Ala Tyr Met Asn Cys Asn  
 195 200 205  
 Leu Tyr His Tyr Val Pro Asn Asn Asn Ser Ile Cys Asn Thr Lys Asn  
 210 215 220  
 Glu Val Leu Val Lys Asn Asn Ile Gln Glu Leu Gln Leu Val Leu Asn  
 225 230 235 240  
 Tyr Leu Arg Gln Asn Tyr Ile Leu Asn Lys Tyr Cys Ser Val Leu Tyr  
 245 250 255  
 Val Leu Ile Lys Tyr Leu Leu Tyr Ile Gln Ile Tyr Lys Ile Lys Arg  
 260 265 270  
 Thr Lys Leu Met Val Thr Leu Leu Ala Lys Ile Asn Ile Leu Thr Leu  
 275 280 285  
 Lys Ile Leu Phe Lys Tyr Lys Lys Phe Leu Lys Gln Cys  
 290 295 300

<210> 28  
 <211> 912  
 <212> DNA  
 <213> Campylobacter jejuni

<220>  
 <221> CDS  
 <222> (1)..(912)  
 <223> Campylobacter glycosyltransferase B (CgtB) beta-1,3  
 galactosyltransferase from C. jejuni serotype O:2  
 (strain NCTC 11168)

<400> 28  
atg agt caa att tcc atc ata cta cca act tat aat gtg gaa aaa tat 48  
Met Ser Gln Ile Ser Ile Ile Leu Pro Thr Tyr Asn Val Glu Lys Tyr  
1 5 10 15

att gct aga gca tta gaa agt tgc att aac caa act ttt aaa gat ata 96  
Ile Ala Arg Ala Leu Glu Ser Cys Ile Asn Gln Thr Phe Lys Asp Ile  
20 25 30

gaa atc att gta gta gat gat tgt ggt aat gat aaa agt ata gat ata 144  
Glu Ile Ile Val Val Asp Asp Cys Gly Asn Asp Lys Ser Ile Asp Ile  
35 40 45

gct aaa gag tat gct agt aaa gat gat aga ata aaa atc ata cat aat 192  
Ala Lys Glu Tyr Ala Ser Lys Asp Asp Arg Ile Lys Ile Ile His Asn  
50 55 60

gaa gag aat tta aag ctt tta aga gca aga tat gaa ggt gct aaa gta 240  
Glu Glu Asn Leu Lys Leu Leu Arg Ala Arg Tyr Glu Gly Ala Lys Val  
65 70 75 80

gca act tca cct tat atc atg ttt tta gat tct gat gat tat tta gaa 288  
Ala Thr Ser Pro Tyr Ile Met Phe Leu Asp Ser Asp Asp Tyr Leu Glu  
85 90 95

ctt aat gct tgc gaa gaa tgt att aaa att ttg gat atg ggt ggg ggg 336  
Leu Asn Ala Cys Glu Glu Cys Ile Lys Ile Leu Asp Met Gly Gly Gly  
100 105 110

ggt aaa att gat ttg ttg tgt ttt gaa gct ttt att acc aat gca aaa 384  
Gly Lys Ile Asp Leu Leu Cys Phe Glu Ala Phe Ile Thr Asn Ala Lys  
115 120 125

aaa tca ata aaa aaa tta aat ata aaa caa gga aaa tac aac aac aaa 432  
Lys Ser Ile Lys Lys Leu Asn Ile Lys Gln Gly Lys Tyr Asn Asn Lys  
130 135 140

gaa ttt aca atg caa ata ctt aaa act aaa aat cca ttt tgg aca atg 480  
Glu Phe Thr Met Gln Ile Leu Lys Thr Lys Asn Pro Phe Trp Thr Met  
145 150 155 160

tgg gct aaa ata atc aaa aaa gat att tat tta aaa gcc ttc aac atg 528  
Trp Ala Lys Ile Ile Lys Lys Asp Ile Tyr Leu Lys Ala Phe Asn Met  
165 170 175

tta aat ctc aaa aaa gaa atc aaa ata aat atg gca gaa gat gcc tta 576  
Leu Asn Leu Lys Lys Glu Ile Lys Ile Asn Met Ala Glu Asp Ala Leu  
180 185 190

tta tat tat cct ttg aca ata tta tct aat gaa ata ttt tac tta aca 624  
Leu Tyr Tyr Pro Leu Thr Ile Leu Ser Asn Glu Ile Phe Tyr Leu Thr  
195 200 205

caa cct ttg tat acc cag cat gta aat agc aat tct ata aca aat aat 672  
Gln Pro Leu Tyr Thr Gln His Val Asn Ser Asn Ser Ile Thr Asn Asn  
210 215 220

att aat tct tta gaa gct aat att caa gaa cat aaa att gtt tta aat 720  
Ile Asn Ser Leu Glu Ala Asn Ile Gln Glu His Lys Ile Val Leu Asn  
225 230 235 240

gtt tta aaa tca att aaa aat aaa aaa aca cct cta tat ttt cta att 768  
 Val Leu Lys Ser Ile Lys Asn Lys Lys Thr Pro Leu Tyr Phe Leu Ile  
                   245                                  250                                  255

ata tat tta tta aaa att caa tta ttg aaa tat gaa caa aat ttt aat 816  
 Ile Tyr Leu Leu Lys Ile Gln Leu Leu Lys Tyr Glu Gln Asn Phe Asn  
                   260                                  265                                  270

aaa aga aat ata aat ctt att tat tat aaa ata aat att tta tat caa 864  
 Lys Arg Asn Ile Asn Leu Ile Tyr Tyr Lys Ile Asn Ile Leu Tyr Gln  
                   275                                  280                                  285

aaa tat caa ttc aaa tgg aaa aaa ttt tta tat aat tta att ccg taa 912  
 Lys Tyr Gln Phe Lys Trp Lys Lys Phe Leu Tyr Asn Leu Ile Pro  
                   290                                  295                                  300

<210> 29

<211> 303

<212> PRT

<213> Campylobacter jejuni

<220>

<223> Campylobacter glycosyltransferase B (CgtB) beta-1,3  
 galactosyltransferase from C. jejuni serotype O:2  
 (strain NCTC 11168)

<400> 29

Met Ser Gln Ile Ser Ile Ile Leu Pro Thr Tyr Asn Val Glu Lys Tyr  
   1                                  5                                  10                                  15  
 Ile Ala Arg Ala Leu Glu Ser Cys Ile Asn Gln Thr Phe Lys Asp Ile  
                   20                                  25                                  30  
 Glu Ile Ile Val Val Asp Asp Cys Gly Asn Asp Lys Ser Ile Asp Ile  
                   35                                  40                                  45  
 Ala Lys Glu Tyr Ala Ser Lys Asp Asp Arg Ile Lys Ile Ile His Asn  
                   50                                  55                                  60  
 Glu Glu Asn Leu Lys Leu Leu Arg Ala Arg Tyr Glu Gly Ala Lys Val  
                   65                                  70                                  75                                  80  
 Ala Thr Ser Pro Tyr Ile Met Phe Leu Asp Ser Asp Asp Tyr Leu Glu  
                   85                                  90                                  95  
 Leu Asn Ala Cys Glu Glu Cys Ile Lys Ile Leu Asp Met Gly Gly Gly  
                   100                                  105                                  110  
 Gly Lys Ile Asp Leu Leu Cys Phe Glu Ala Phe Ile Thr Asn Ala Lys  
                   115                                  120                                  125  
 Lys Ser Ile Lys Lys Leu Asn Ile Lys Gln Gly Lys Tyr Asn Asn Lys  
                   130                                  135                                  140  
 Glu Phe Thr Met Gln Ile Leu Lys Thr Lys Asn Pro Phe Trp Thr Met  
                   145                                  150                                  155                                  160  
 Trp Ala Lys Ile Ile Lys Lys Asp Ile Tyr Leu Lys Ala Phe Asn Met  
                   165                                  170                                  175  
 Leu Asn Leu Lys Lys Glu Ile Lys Ile Asn Met Ala Glu Asp Ala Leu  
                   180                                  185                                  190  
 Leu Tyr Tyr Pro Leu Thr Ile Leu Ser Asn Glu Ile Phe Tyr Leu Thr  
                   195                                  200                                  205  
 Gln Pro Leu Tyr Thr Gln His Val Asn Ser Asn Ser Ile Thr Asn Asn  
                   210                                  215                                  220  
 Ile Asn Ser Leu Glu Ala Asn Ile Gln Glu His Lys Ile Val Leu Asn  
                   225                                  230                                  235                                  240  
 Val Leu Lys Ser Ile Lys Asn Lys Lys Thr Pro Leu Tyr Phe Leu Ile  
                   245                                  250                                  255

Ile Tyr Leu Leu Lys Ile Gln Leu Leu Lys Tyr Glu Gln Asn Phe Asn  
260 265 270  
Lys Arg Asn Ile Asn Leu Ile Tyr Tyr Lys Ile Asn Ile Leu Tyr Gln  
275 280 285  
Lys Tyr Gln Phe Lys Trp Lys Lys Phe Leu Tyr Asn Leu Ile Pro  
290 295 300

<210> 30  
<211> 891  
<212> DNA  
<213> Campylobacter jejuni

<220>  
<221> CDS  
<222> (1)..(891)  
<223> beta-1,3 galactosyl transferase from C. jejuni O:10

<400> 30  
atg ttt aaa att tca atc atc ttg cca act tat aat gtg gaa caa tat 48  
Met Phe Lys Ile Ser Ile Ile Leu Pro Thr Tyr Asn Val Glu Gln Tyr  
1 5 10 15  
ata gca agg gca ata gaa agt tgt atc aat cag act ttt aaa aat ata 96  
Ile Ala Arg Ala Ile Glu Ser Cys Ile Asn Gln Thr Phe Lys Asn Ile  
20 25 30  
gaa ata att gta gtt gat gat tgt gga agt gac aaa agt ata gat ata 144  
Glu Ile Ile Val Val Asp Asp Cys Gly Ser Asp Lys Ser Ile Asp Ile  
35 40 45  
gtt aaa gaa tat gcc aaa aaa gat gat aga ata aaa atc ata cat aat 192  
Val Lys Glu Tyr Ala Lys Lys Asp Asp Arg Ile Lys Ile Ile His Asn  
50 55 60  
gaa gaa aat tta aaa ctt tta aga gct aga tat gaa ggt gta aaa gta 240  
Glu Glu Asn Leu Lys Leu Leu Arg Ala Arg Tyr Glu Gly Val Lys Val  
65 70 75 80  
gca aac tct cct tat ata atg ttt tta gat cct gat gat tat tta gaa 288  
Ala Asn Ser Pro Tyr Ile Met Phe Leu Asp Pro Asp Asp Tyr Leu Glu  
85 90 95  
ctt aat gct tgt gaa gaa tgt atg aaa att tta aaa aac aat gaa ata 336  
Leu Asn Ala Cys Glu Glu Cys Met Lys Ile Leu Lys Asn Asn Glu Ile  
100 105 110  
gat tta tta ttt ttt aat gca ttt gta ttg gaa aat aac aat aaa ata 384  
Asp Leu Leu Phe Phe Asn Ala Phe Val Leu Glu Asn Asn Asn Lys Ile  
115 120 125  
gaa aga aag ttg aat ttt caa gaa aaa tgt tat gta aaa aaa gat ttt 432  
Glu Arg Lys Leu Asn Phe Gln Glu Lys Cys Tyr Val Lys Lys Asp Phe  
130 135 140  
tta aaa gaa cta tta aaa act aaa aat tta ttt tgg aca gtg tgg gca 480  
Leu Lys Glu Leu Leu Lys Thr Lys Asn Leu Phe Trp Thr Val Trp Ala  
145 150 155 160



aaa gtc ata aaa aaa gaa tta tat ctc aag gct gtt ggt tta ata tcg 528  
 Lys Val Ile Lys Lys Glu Leu Tyr Leu Lys Ala Val Gly Leu Ile Ser  
 165 170 175  
  
 cta gaa aat gct aaa ata aat atg gct gaa gat gtt tta tta tat tac 576  
 Leu Glu Asn Ala Lys Ile Asn Met Ala Glu Asp Val Leu Leu Tyr Tyr  
 180 185 190  
  
 cct ttg ata aat att tca aat act ata ttt cac ttg agt aaa aat tta 624  
 Pro Leu Ile Asn Ile Ser Asn Thr Ile Phe His Leu Ser Lys Asn Leu  
 195 200 205  
  
 tac aat tat caa ata aat aat ttc tct ata acc aaa aca tta aca ttg 672  
 Tyr Asn Tyr Gln Ile Asn Asn Phe Ser Ile Thr Lys Thr Leu Thr Leu  
 210 215 220  
  
 caa aat ata aaa aca aat ata caa gaa caa gat aat gtt cta tat ctt 720  
 Gln Asn Ile Lys Thr Asn Ile Gln Glu Gln Asp Asn Val Leu Tyr Leu  
 225 230 235 240  
  
 cta aag aag atg caa tat aat tac aat ttt aac tta act ttg ctt aaa 768  
 Leu Lys Lys Met Gln Tyr Asn Tyr Asn Phe Asn Leu Thr Leu Leu Lys  
 245 250 255  
  
 tta att gag tat ttt tta tta att gaa aaa tac tca tta tca agc aag 816  
 Leu Ile Glu Tyr Phe Leu Leu Ile Glu Lys Tyr Ser Leu Ser Ser Lys  
 260 265 270  
  
 cga aat gtt ctt tgt ttt aaa atc aat att ttt ttt aaa aaa atc caa 864  
 Arg Asn Val Leu Cys Phe Lys Ile Asn Ile Phe Phe Lys Lys Ile Gln  
 275 280 285  
  
 ttt aaa ttt tat cgc ttg ctg aag atg 891  
 Phe Lys Phe Tyr Arg Leu Leu Lys Met  
 290 295

<210> 31  
 <211> 297  
 <212> PRT  
 <213> Campylobacter jejuni

<220>  
 <223> beta-1,3 galactosyl transferase from C. jejuni O:10

<400> 31  
 Met Phe Lys Ile Ser Ile Ile Leu Pro Thr Tyr Asn Val Glu Gln Tyr  
 1 5 10 15  
 Ile Ala Arg Ala Ile Glu Ser Cys Ile Asn Gln Thr Phe Lys Asn Ile  
 20 25 30  
 Glu Ile Ile Val Val Asp Asp Cys Gly Ser Asp Lys Ser Ile Asp Ile  
 35 40 45  
 Val Lys Glu Tyr Ala Lys Lys Asp Asp Arg Ile Lys Ile Ile His Asn  
 50 55 60  
 Glu Glu Asn Leu Lys Leu Leu Arg Ala Arg Tyr Glu Gly Val Lys Val  
 65 70 75 80  
 Ala Asn Ser Pro Tyr Ile Met Phe Leu Asp Pro Asp Asp Tyr Leu Glu  
 85 90 95  
 Leu Asn Ala Cys Glu Glu Cys Met Lys Ile Leu Lys Asn Asn Glu Ile  
 100 105 110

Asp Leu Leu Phe Phe Asn Ala Phe Val Leu Glu Asn Asn Asn Lys Ile  
 115 120 125  
 Glu Arg Lys Leu Asn Phe Gln Glu Lys Cys Tyr Val Lys Lys Asp Phe  
 130 135 140  
 Leu Lys Glu Leu Leu Lys Thr Lys Asn Leu Phe Trp Thr Val Trp Ala  
 145 150 155 160  
 Lys Val Ile Lys Lys Glu Leu Tyr Leu Lys Ala Val Gly Leu Ile Ser  
 165 170 175  
 Leu Glu Asn Ala Lys Ile Asn Met Ala Glu Asp Val Leu Leu Tyr Tyr  
 180 185 190  
 Pro Leu Ile Asn Ile Ser Asn Thr Ile Phe His Leu Ser Lys Asn Leu  
 195 200 205  
 Tyr Asn Tyr Gln Ile Asn Asn Phe Ser Ile Thr Lys Thr Leu Thr Leu  
 210 215 220  
 Gln Asn Ile Lys Thr Asn Ile Gln Glu Gln Asp Asn Val Leu Tyr Leu  
 225 230 235 240  
 Leu Lys Lys Met Gln Tyr Asn Tyr Asn Phe Asn Leu Thr Leu Leu Lys  
 245 250 255  
 Leu Ile Glu Tyr Phe Leu Leu Ile Glu Lys Tyr Ser Leu Ser Ser Lys  
 260 265 270  
 Arg Asn Val Leu Cys Phe Lys Ile Asn Ile Phe Phe Lys Lys Ile Gln  
 275 280 285  
 Phe Lys Phe Tyr Arg Leu Leu Lys Met  
 290 295

<210> 32

<211> 295

<212> PRT

<213> Campylobacter jejuni

<220>

<223> lipid A biosynthesis acyltransferase from C.  
 jejuni OH4384

<400> 32

Met Lys Asn Ser Asp Arg Ile Tyr Leu Ser Leu Tyr Tyr Ile Leu Lys  
 1 5 10 15  
 Phe Phe Val Thr Phe Met Pro Asp Cys Ile Leu His Phe Leu Ala Leu  
 20 25 30  
 Ile Val Ala Arg Ile Ala Phe His Leu Asn Lys Lys His Arg Lys Ile  
 35 40 45  
 Ile Asn Thr Asn Leu Gln Ile Cys Phe Pro Gln Tyr Thr Gln Lys Glu  
 50 55 60  
 Arg Asp Lys Leu Ser Leu Lys Ile Tyr Glu Asn Phe Ala Gln Phe Gly  
 65 70 75 80  
 Ile Asp Cys Leu Gln Asn Gln Asn Thr Thr Lys Glu Lys Ile Leu Asn  
 85 90 95  
 Lys Val Asn Phe Ile Asn Glu Asn Phe Leu Ile Asp Ala Leu Ala Leu  
 100 105 110  
 Lys Arg Pro Ile Ile Phe Thr Thr Ala His Tyr Gly Asn Trp Glu Ile  
 115 120 125  
 Leu Ser Leu Ala Tyr Ala Ala Lys Tyr Gly Ala Ile Ser Ile Val Gly  
 130 135 140  
 Lys Lys Leu Lys Ser Glu Val Met Tyr Glu Ile Leu Ser Gln Ser Arg  
 145 150 155 160  
 Thr Gln Phe Asp Ile Glu Leu Ile Asp Lys Lys Gly Gly Ile Arg Gln  
 165 170 175  
 Met Leu Ser Ala Leu Lys Lys Glu Arg Ala Leu Gly Ile Leu Thr Asp  
 180 185 190

Gln Asp Cys Val Glu Asn Glu Ser Val Arg Leu Lys Phe Phe Asn Lys  
           195                          200                          205  
 Glu Val Asn Tyr Gln Met Gly Ala Ser Leu Ile Ala Gln Arg Ser Asn  
           210                          215                          220  
 Ala Leu Ile Ile Pro Val Tyr Ala Tyr Lys Glu Gly Gly Lys Phe Cys  
 225                          230                          235                          240  
 Ile Glu Phe Phe Lys Ala Lys Asp Ser Gln Asn Ala Ser Leu Glu Glu  
                           245                          250                          255  
 Leu Thr Leu Tyr Gln Ala Gln Ser Cys Glu Glu Met Ile Lys Lys Arg  
                           260                          265                          270  
 Pro Trp Glu Tyr Phe Phe Phe His Arg Arg Phe Ala Ser Tyr Asn Glu  
           275                          280                          285  
 Glu Ile Tyr Lys Gly Ala Lys  
           290                          295

<210> 33

<211> 418

<212> PRT

<213> Campylobacter jejuni

<220>

<223> glycosyltransferase from C. jejuni OH4384 (ORF 3a  
of lipooligosaccharide (LOS) biosynthesis locus)

<400> 33

Met Asn Leu Lys Gln Ile Ser Val Ile Ile Ile Val Lys Asn Ala Glu  
   1                          5                          10                          15  
 Gln Thr Leu Leu Glu Cys Leu Asn Ser Leu Lys Asp Phe Asp Glu Ile  
           20                          25                          30  
 Ile Leu Leu Asn Asn Glu Ser Ser Asp Asn Thr Leu Lys Ile Ala Asn  
           35                          40                          45  
 Glu Phe Lys Lys Asp Phe Ala Asn Leu Tyr Ile Tyr His Asn Ala Phe  
           50                          55                          60  
 Ile Gly Phe Gly Ala Leu Lys Asn Leu Ala Leu Ser Tyr Ala Lys Asn  
           65                          70                          75                          80  
 Asp Trp Ile Leu Ser Ile Asp Ala Asp Glu Val Leu Glu Asn Glu Cys  
                           85                          90                          95  
 Ile Lys Glu Leu Lys Asn Leu Lys Leu Gln Glu Asp Asn Ile Ile Ala  
           100                          105                          110  
 Leu Ser Arg Lys Asn Leu Tyr Lys Gly Glu Trp Ile Lys Ala Cys Gly  
           115                          120                          125  
 Trp Trp Pro Asp Tyr Val Leu Arg Ile Phe Asn Lys Asn Phe Thr Arg  
           130                          135                          140  
 Phe Asn Asp Asn Leu Val His Glu Ser Leu Val Leu Pro Ser Asn Ala  
           145                          150                          155                          160  
 Lys Lys Ile Tyr Leu Lys Asn Gly Leu Lys His Tyr Ser Tyr Lys Asp  
                           165                          170                          175  
 Ile Ser His Leu Ile Asp Lys Met Gln Tyr Tyr Ser Ser Leu Trp Ala  
           180                          185                          190  
 Lys Gln Asn Ile His Lys Lys Ser Gly Val Leu Lys Ala Asn Leu Arg  
           195                          200                          205  
 Ala Phe Trp Thr Phe Phe Arg Asn Tyr Phe Leu Lys Asn Gly Phe Leu  
           210                          215                          220  
 Tyr Gly Tyr Lys Gly Phe Ile Ile Ser Val Cys Ser Ala Leu Gly Thr  
           225                          230                          235                          240  
 Phe Phe Lys Tyr Met Lys Leu Tyr Glu Leu Gln Arg Gln Lys Pro Lys  
                           245                          250                          255  
 Thr Cys Ala Leu Ile Ile Ile Thr Tyr Asn Gln Lys Glu Arg Leu Lys  
           260                          265                          270

Leu Val Leu Asp Ser Val Lys Asn Leu Ala Phe Leu Pro Asn Glu Val  
           275                          280                          285  
 Leu Ile Ala Asp Asp Gly Ser Lys Glu Asp Thr Ala Arg Leu Ile Glu  
           290                          295                          300  
 Glu Tyr Gln Lys Asp Phe Pro Cys Pro Leu Lys His Ile Trp Gln Glu  
 305                          310                          315                          320  
 Asp Glu Gly Phe Lys Leu Ser Lys Ser Arg Asn Lys Thr Ile Lys Asn  
                           325                          330                          335  
 Ala Asp Ser Glu Tyr Ile Ile Val Ile Asp Gly Asp Met Ile Leu Glu  
                           340                          345                          350  
 Lys Asp Phe Ile Lys Glu His Leu Glu Phe Ala Gln Arg Lys Leu Phe  
                           355                          360                          365  
 Leu Gln Gly Ser Arg Val Ile Leu Asn Lys Lys Glu Ser Glu Glu Ile  
           370                          375                          380  
 Leu Asn Lys Asp Asp Tyr Arg Ile Ile Phe Asn Lys Lys Asp Phe Lys  
 385                          390                          395                          400  
 Ser Ser Lys Asn Ser Phe Leu Ala Lys Ile Phe Tyr Ser Leu Ser Lys  
                           405                          410                          415  
 Lys Arg

<210> 34  
 <211> 389  
 <212> PRT  
 <213> Campylobacter jejuni

<220>  
 <223> glycosyltransferase of C. jejuni OH4384 (ORF 4a of  
         lipooligosaccharide (LOS) biosynthesis locus)

<400> 34  
 Met Lys Lys Ile Gly Val Val Ile Pro Ile Tyr Asn Val Glu Lys Tyr  
   1                          5                          10                          15  
 Leu Arg Glu Cys Leu Asp Ser Val Ile Asn Gln Thr Tyr Thr Asn Leu  
           20                          25                          30  
 Glu Ile Ile Leu Val Asn Asp Gly Ser Thr Asp Glu His Ser Leu Asn  
           35                          40                          45  
 Ile Ala Lys Glu Tyr Thr Leu Lys Asp Lys Arg Ile Thr Leu Phe Asp  
           50                          55                          60  
 Lys Lys Asn Gly Gly Leu Ser Ser Ala Arg Asn Ile Gly Ile Glu Tyr  
 65                          70                          75                          80  
 Phe Ser Gly Glu Tyr Lys Leu Lys Asn Lys Thr Gln His Ile Lys Glu  
                           85                          90                          95  
 Asn Ser Leu Ile Glu Phe Gln Leu Asp Gly Asn Asn Pro Tyr Asn Ile  
           100                          105                          110  
 Tyr Lys Ala Tyr Lys Ser Ser Gln Ala Phe Asn Asn Glu Lys Asp Leu  
           115                          120                          125  
 Thr Asn Phe Thr Tyr Pro Ser Ile Asp Tyr Ile Ile Phe Leu Asp Ser  
           130                          135                          140  
 Asp Asn Tyr Trp Lys Leu Asn Cys Ile Glu Glu Cys Val Ile Arg Met  
 145                          150                          155                          160  
 Lys Asn Val Asp Val Leu Trp Phe Asp His Asp Cys Thr Tyr Glu Asp  
                           165                          170                          175  
 Asn Ile Lys Asn Lys His Lys Lys Thr Arg Met Glu Ile Phe Asp Phe  
           180                          185                          190  
 Lys Lys Glu Cys Ile Ile Thr Pro Lys Glu Tyr Ala Asn Arg Ala Leu  
           195                          200                          205  
 Ser Val Gly Ser Arg Asp Ile Ser Phe Gly Trp Asn Gly Met Ile Asp  
           210                          215                          220  
 Phe Asn Phe Leu Lys Gln Ile Lys Leu Lys Phe Ile Asn Phe Ile Ile  
 225                          230                          235                          240



Gly	Ala	Cys	Val	Leu	Glu	Arg	His	Phe	Thr	Asp	Ser	Met	His	Arg	Ser
225					230					235					240
Gly	Pro	Asp	Ile	Val	Cys	Ser	Met	Asp	Thr	Gln	Ala	Leu	Lys	Glu	Leu
			245						250					255	
Ile	Ile	Gln	Ser	Glu	Gln	Met	Ala	Ile	Met	Arg	Gly	Asn	Asn	Glu	Ser
		260						265					270		
Lys	Lys	Ala	Ala	Lys	Gln	Glu	Gln	Val	Thr	Ile	Asp	Phe	Ala	Phe	Ala
		275					280					285			
Ser	Val	Val	Ser	Ile	Lys	Asp	Ile	Lys	Lys	Gly	Glu	Val	Leu	Ser	Met
	290					295					300				
Asp	Asn	Ile	Trp	Val	Lys	Arg	Pro	Gly	Leu	Gly	Gly	Ile	Ser	Ala	Ala
305					310					315					320
Glu	Phe	Glu	Asn	Ile	Leu	Gly	Lys	Lys	Ala	Leu	Arg	Asp	Ile	Glu	Asn
			325						330					335	
Asp	Thr	Gln	Leu	Ser	Tyr	Glu	Asp	Phe	Ala						
			340						345						

<210> 36

<211> 352

<212> PRT

<213> Campylobacter jejuni

<220>

<223> enzyme involved in sialic acid biosynthesis from  
C. jejuni OH4384 (ORF 9a of lipooligosaccharide (LOS)  
biosynthesis locus)

<400> 36

Met	Tyr	Arg	Val	Gln	Asn	Ser	Ser	Glu	Phe	Glu	Leu	Tyr	Ile	Phe	Ala
1				5					10					15	
Thr	Gly	Met	His	Leu	Ser	Lys	Asn	Phe	Gly	Tyr	Thr	Val	Lys	Glu	Leu
			20					25					30		
Tyr	Lys	Asn	Gly	Phe	Lys	Asn	Ile	Tyr	Glu	Phe	Ile	Asn	Tyr	Asp	Lys
		35				40						45			
Tyr	Phe	Ser	Thr	Asp	Lys	Ala	Leu	Ala	Thr	Thr	Ile	Asp	Gly	Phe	Ser
	50					55					60				
Arg	Tyr	Val	Asn	Glu	Leu	Lys	Pro	Asp	Leu	Ile	Val	Val	His	Gly	Asp
65					70					75					80
Arg	Ile	Glu	Pro	Leu	Ala	Ala	Ala	Ile	Val	Gly	Ala	Leu	Asn	Asn	Ile
				85					90					95	
Leu	Val	Ala	His	Ile	Glu	Gly	Gly	Glu	Ile	Ser	Gly	Thr	Ile	Asp	Asp
			100					105					110		
Ser	Leu	Arg	His	Ala	Ile	Ser	Lys	Leu	Ala	His	Ile	His	Leu	Val	Asn
		115					120					125			
Asp	Glu	Phe	Ala	Lys	Arg	Arg	Leu	Met	Gln	Leu	Gly	Glu	Asp	Glu	Lys
	130					135					140				
Ser	Ile	Phe	Ile	Ile	Gly	Ser	Pro	Asp	Leu	Glu	Leu	Leu	Asn	Asp	Asn
145					150					155				160	
Lys	Ile	Ser	Leu	Asn	Glu	Ala	Lys	Lys	Tyr	Tyr	Asp	Ile	Asn	Tyr	Glu
				165					170					175	
Asn	Tyr	Ala	Leu	Leu	Met	Phe	His	Pro	Val	Thr	Thr	Glu	Ile	Thr	Ser
		180						185					190		
Ile	Lys	Asn	Gln	Ala	Asp	Asn	Leu	Val	Lys	Ala	Leu	Ile	Gln	Ser	Asn
		195					200					205			
Lys	Asn	Tyr	Ile	Val	Ile	Tyr	Pro	Asn	Asn	Asp	Leu	Gly	Phe	Glu	Leu
	210					215					220				
Ile	Leu	Gln	Ser	Tyr	Glu	Glu	Leu	Lys	Asn	Asn	Pro	Arg	Phe	Lys	Leu
225					230					235					240
Phe	Pro	Ser	Leu	Arg	Phe	Glu	Tyr	Phe	Ile	Thr	Leu	Leu	Lys	Asn	Ala
				245						250				255	

Asp Phe Ile Ile Gly Asn Ser Ser Cys Ile Leu Lys Glu Ala Leu Tyr  
                   260                  265                  270  
 Leu Lys Thr Ala Gly Ile Leu Val Gly Ser Arg Gln Asn Gly Arg Leu  
                   275                  280                  285  
 Gly Asn Glu Asn Thr Leu Lys Val Asn Ala Asn Ser Asp Glu Ile Leu  
                   290                  295                  300  
 Lys Ala Ile Asn Thr Ile His Lys Lys Gln Asp Leu Phe Ser Ala Lys  
 305                  310                  315                  320  
 Leu Glu Ile Leu Asp Ser Ser Lys Leu Phe Phe Glu Tyr Leu Gln Ser  
                   325                  330                  335  
 Gly Glu Phe Phe Lys Leu Asn Thr Gln Lys Val Phe Lys Asp Ile Lys  
                   340                  345                  350

<210> 37

<211> 221

<212> PRT

<213> Campylobacter jejuni

<220>

<223> CMP-sialic acid synthetase from C. jejuni OH4384  
 (ORF 10a of lipooligosaccharide (LOS) biosynthesis  
 locus)

<400> 37

Met Ser Leu Ala Ile Ile Pro Ala Arg Gly Gly Ser Lys Gly Ile Lys  
   1                  5                  10                  15  
 Asn Lys Asn Leu Val Leu Leu Asn Asn Lys Pro Leu Ile Tyr Tyr Thr  
                   20                  25                  30  
 Ile Lys Ala Ala Leu Asn Thr Lys Ser Ile Ser Lys Val Val Val Ser  
                   35                  40                  45  
 Ser Asp Ser Asp Glu Ile Leu Asn Tyr Ala Lys Ser Gln Asn Val Asp  
                   50                  55                  60  
 Ile Leu Lys Arg Pro Ile Ser Leu Ala Gln Asp Asn Thr Thr Ser Asp  
                   65                  70                  75                  80  
 Lys Val Leu Leu His Ala Leu Lys Phe Tyr Lys Asp Tyr Glu Asp Val  
                   85                  90                  95  
 Val Phe Leu Gln Pro Thr Ser Pro Leu Arg Thr Asn Ile His Ile Asp  
                   100                  105                  110  
 Glu Ala Phe Asn Leu Tyr Lys Asn Ser Asn Ala Asn Ala Leu Ile Ser  
                   115                  120                  125  
 Val Ser Glu Cys Asp Asn Lys Ile Leu Lys Ala Phe Val Cys Asn Glu  
                   130                  135                  140  
 Tyr Gly Asp Leu Ala Gly Ile Cys Asn Asp Glu Tyr Pro Phe Met Pro  
 145                  150                  155                  160  
 Arg Gln Lys Leu Pro Lys Thr Tyr Met Ser Asn Gly Ala Ile Tyr Ile  
                   165                  170                  175  
 Leu Lys Ile Lys Glu Phe Leu Asn Asn Pro Ser Phe Leu Gln Ser Lys  
                   180                  185                  190  
 Thr Lys His Phe Leu Met Asp Glu Ser Ser Ser Leu Asp Ile Asp Cys  
                   195                  200                  205  
 Leu Glu Asp Leu Lys Lys Ala Glu Gln Ile Trp Lys Lys  
                   210                  215                  220

<210> 38

<211> 277

<212> PRT

<213> Campylobacter jejuni

<220>

<223> acetyltransferase from *C. jejuni* OH4384 (ORF 11a  
of lipooligosaccharide (LOS) biosynthesis locus)

<400> 38

```
Met Glu Lys Ile Thr Leu Lys Cys Asn Lys Asn Ile Leu Asn Leu Leu
  1           5           10           15
Lys Gln Tyr Asn Ile Tyr Thr Lys Thr Tyr Ile Glu Asn Pro Arg Arg
          20           25           30
Phe Ser Arg Leu Lys Thr Lys Asp Phe Ile Thr Phe Pro Leu Glu Asn
          35           40           45
Asn Gln Leu Glu Ser Val Ala Gly Leu Gly Ile Glu Glu Tyr Cys Ala
          50           55           60
Phe Lys Phe Ser Asn Ile Leu His Glu Met Asp Ser Phe Ser Phe Ser
          65           70           75           80
Gly Ser Phe Leu Pro His Tyr Thr Lys Val Gly Arg Tyr Cys Ser Ile
          85           90           95
Ser Asp Gly Val Ser Met Phe Asn Phe Gln His Pro Met Asp Arg Ile
          100          105          110
Ser Thr Ala Ser Phe Thr Tyr Glu Thr Asn His Ser Phe Ile Asn Asp
          115          120          125
Ala Cys Gln Asn His Ile Asn Lys Thr Phe Pro Ile Val Asn His Asn
          130          135          140
Pro Ser Ser Ser Ile Thr His Leu Ile Ile Gln Asp Asp Val Trp Ile
          145          150          155          160
Gly Lys Asp Val Leu Leu Lys Gln Gly Ile Thr Leu Gly Thr Gly Cys
          165          170          175
Val Ile Gly Gln Arg Ala Val Val Thr Lys Asp Val Pro Pro Tyr Ala
          180          185          190
Ile Val Ala Gly Ile Pro Ala Lys Ile Ile Lys Tyr Arg Phe Asp Glu
          195          200          205
Lys Thr Ile Glu Arg Leu Leu Lys Ile Gln Trp Trp Lys Tyr His Phe
          210          215          220
Ala Asp Phe Tyr Asp Ile Asp Leu Asn Leu Lys Ile Asn Gln Tyr Leu
          225          230          235          240
Asp Leu Leu Glu Glu Lys Ile Ile Lys Lys Ser Ile Ser Tyr Tyr Asn
          245          250          255
Pro Asn Lys Leu Tyr Phe Arg Asp Ile Leu Glu Leu Lys Ser Lys Lys
          260          265          270
Ile Phe Asn Leu Phe
          275
```

<210> 39

<211> 270

<212> PRT

<213> *Campylobacter jejuni*

<220>

<223> glycosyltransferase from *C. jejuni* OH4384 (ORF 12a  
of lipooligosaccharide (LOS) biosynthesis locus)

<400> 39

```
Met Pro Gln Leu Ser Ile Ile Ile Pro Leu Phe Asn Ser Cys Asp Phe
  1           5           10           15
Ile Ser Arg Ala Leu Gln Ser Cys Ile Asn Gln Thr Leu Lys Asp Ile
          20           25           30
Glu Ile Leu Ile Ile Asp Asp Lys Ser Lys Asp Asn Ser Leu Asn Met
          35           40           45
Val Leu Glu Phe Ala Lys Lys Asp Pro Arg Ile Lys Ile Phe Gln Asn
          50           55           60
```



Glu	Glu	Asn	Leu	Gly	Thr	Phe	Ala	Ser	Arg	Asn	Leu	Gly	Val	Leu	His
65					70					75					80
Ser	Ser	Ser	Asp	Phe	Ile	Met	Phe	Leu	Asp	Ser	Asp	Asp	Phe	Leu	Thr
			85						90					95	
Pro	Asp	Ala	Cys	Glu	Ile	Ala	Phe	Lys	Glu	Met	Lys	Lys	Gly	Phe	Asp
			100					105					110		
Leu	Leu	Cys	Phe	Asp	Ala	Phe	Val	His	Arg	Val	Lys	Thr	Lys	Gln	Phe
		115					120					125			
Tyr	Arg	Phe	Lys	Gln	Asp	Glu	Val	Phe	Asn	Gln	Lys	Glu	Phe	Leu	Glu
	130					135					140				
Phe	Leu	Ser	Lys	Gln	Arg	His	Phe	Cys	Trp	Ser	Val	Trp	Ala	Lys	Cys
145					150					155					160
Phe	Lys	Lys	Asp	Ile	Ile	Leu	Lys	Ser	Phe	Glu	Lys	Ile	Lys	Ile	Asp
			165						170					175	
Glu	Arg	Leu	Asn	Tyr	Gly	Glu	Asp	Val	Leu	Phe	Cys	Tyr	Ile	Tyr	Phe
			180					185					190		
Met	Phe	Cys	Glu	Lys	Ile	Ala	Val	Phe	Lys	Thr	Cys	Ile	Tyr	His	Tyr
		195					200					205			
Glu	Phe	Asn	Pro	Asn	Gly	Arg	Tyr	Glu	Asn	Lys	Asn	Lys	Glu	Ile	Leu
	210					215					220				
Asn	Gln	Asn	Tyr	His	Asp	Lys	Lys	Lys	Ser	Asn	Glu	Ile	Ile	Lys	Lys
225					230					235					240
Leu	Ser	Lys	Glu	Phe	Ala	His	Asp	Glu	Phe	His	Gln	Lys	Leu	Phe	Glu
			245						250					255	
Val	Leu	Lys	Arg	Glu	Glu	Ala	Gly	Val	Lys	Asn	Arg	Leu	Lys		
			260					265					270		

<210> 40

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:CJ42 primer in  
heptosyltransferase-II used to amplify LPS core  
biosynthesis locus

<400> 40

gccattaccg tatcgcttaa ccagg

25

<210> 41

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:CJ43 primer in  
heptosyltransferase-I used to amplify LPS core  
biosynthesis locus

<400> 41

aaagaatacg aatttgctaa agagg

25

<210> 42

<211> 41

<212> DNA

<213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:CJ-106 3'  
 primer used to amplify and clone ORF 5a

<400> 42  
 cctaggtcga cttaaaacaa tgtaagaat attttttta g 41

<210> 43  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:CJ-157 5'  
 primer used to amplify and clone ORF 5a

<400> 43  
 cttaggaggt catatgctat ttcaatcata ctttgtg 37

<210> 44  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:CJ-105 3'  
 primer used to amplify and clone ORF 6a

<400> 44  
 cctaggtcga cctctaaaaa aaatattctt aacattg 37

<210> 45  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:CJ-133 5'  
 primer used to amplify and clone ORF 6a

<400> 45  
 cttaggaggt catatgttta aaatttcaat catcttacc 39

<210> 46  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:CJ-131 5'  
 primer used to amplify and clone ORF 7a

<400> 46  
 cttaggaggt catatgaaaa aagttattat tgctggaaat g 41

<210> 47  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:CJ-132 3'  
 primer used to amplify and clone ORF 7a

<400> 47  
 cctagggtcga cttattttcc ttgaaataa tgctttatat c

41

<210> 48  
 <211> 322  
 <212> PRT  
 <213> Campylobacter jejuni

<220>  
 <223> Campylobacter alpha-2,3-sialyltransferase I (Cst-I)  
 from C. jejuni OH4384

<400> 48  
 Met Thr Arg Thr Arg Met Glu Asn Glu Leu Ile Val Ser Lys Asn Met  
 1 5 10 15  
 Gln Asn Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Asn Ile Asn  
 20 25 30  
 Tyr Lys Arg Leu Pro Arg Glu Tyr Asp Val Phe Arg Cys Asn Gln Phe  
 35 40 45  
 Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Ile Lys Ala Val Phe  
 50 55 60  
 Phe Asn Pro Gly Val Phe Leu Gln Gln Tyr His Thr Ala Lys Gln Leu  
 65 70 75 80  
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 Ile Thr Ser Gly Val Tyr Met Cys Ala Ile Ala Ile Ala Leu Gly Tyr  
 145 150 155 160  
 Lys Thr Ile Tyr Leu Cys Gly Ile Asp Phe Tyr Glu Gly Asp Val Ile  
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 Tyr Pro Phe Glu Ala Met Ser Thr Asn Ile Lys Thr Ile Phe Pro Gly  
 180 185 190  
 Ile Lys Asp Phe Lys Pro Ser Asn Cys His Ser Lys Glu Tyr Asp Ile  
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 Glu Ala Leu Lys Leu Leu Lys Ser Ile Tyr Lys Val Asn Ile Tyr Ala  
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 Leu Cys Asp Asp Ser Ile Leu Ala Asn His Phe Pro Leu Ser Ile Asn  
 225 230 235 240  
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 245 250 255  
 Asp Ile Leu Leu Thr Asp Asn Thr Pro Gly Val Ser Phe Tyr Lys Asn  
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 Gln Leu Lys Ala Asp Asn Lys Ile Met Leu Asn Phe Tyr Asn Ile Leu  
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 His Ser Lys Asp Asn Leu Ile Lys Phe Leu Asn Lys Glu Ile Ala Val  
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 Val Gln Lys Leu Leu Thr Gln Val Asp Ile Gly His Tyr Tyr Leu Asn  
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 Lys Leu Pro Ala Phe Asp Ala Tyr Leu Gln Tyr Asn Glu Leu Tyr Glu  
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 Asn Lys Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Thr Val  
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 Met Gly Tyr Lys Asp Leu Tyr Leu Thr Gly Ile Asp Phe Tyr Gln Glu  
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 Lys Gly Asn Pro Tyr Ala Phe His His Gln Lys Glu Asn Ile Ile Lys  
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 Met Glu Tyr Asp Leu Asn Ala Leu Tyr Phe Leu Gln Lys His Tyr Gly  
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 Pro Leu Ser Pro Leu Asn Asn Pro Ile Thr Phe Ile Leu Glu Glu Lys  
 165 170 175  
 Lys Asn Tyr Thr Gln Asp Ile Leu Ile Pro Pro Lys Phe Val Tyr Lys  
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 Lys Ile Gly Ile Tyr Ser Lys Pro Arg Ile Tyr Gln Asn Leu Ile Phe  
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 Arg Leu Ile Trp Asp Ile Leu Arg Leu Pro Asn Asp Ile Lys His Ala  
 210 215 220  
 Leu Lys Ser Arg Lys Trp Asp  
 225 230